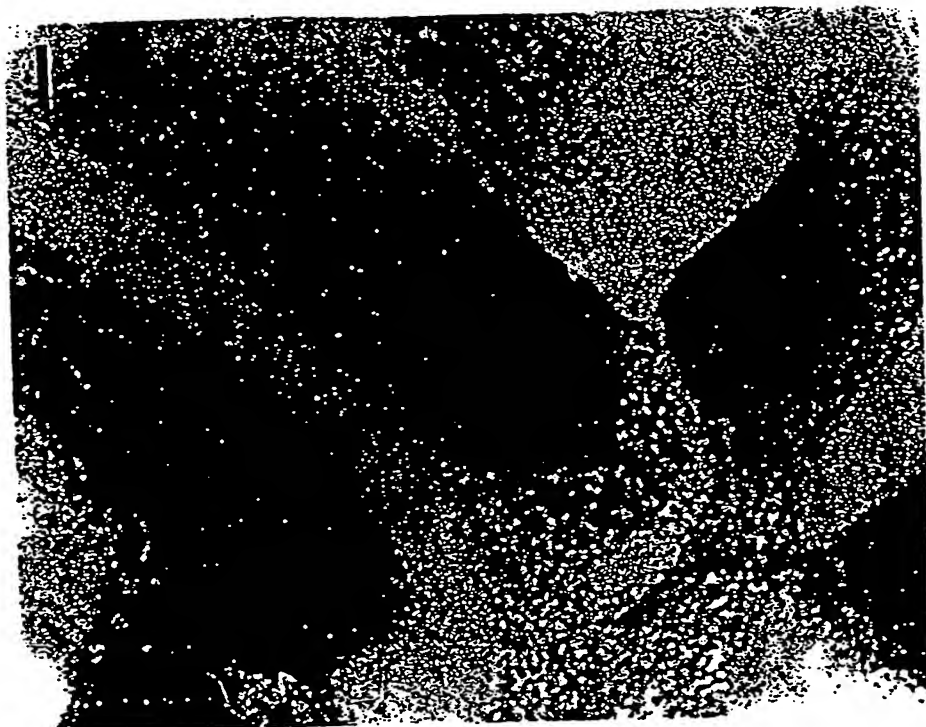
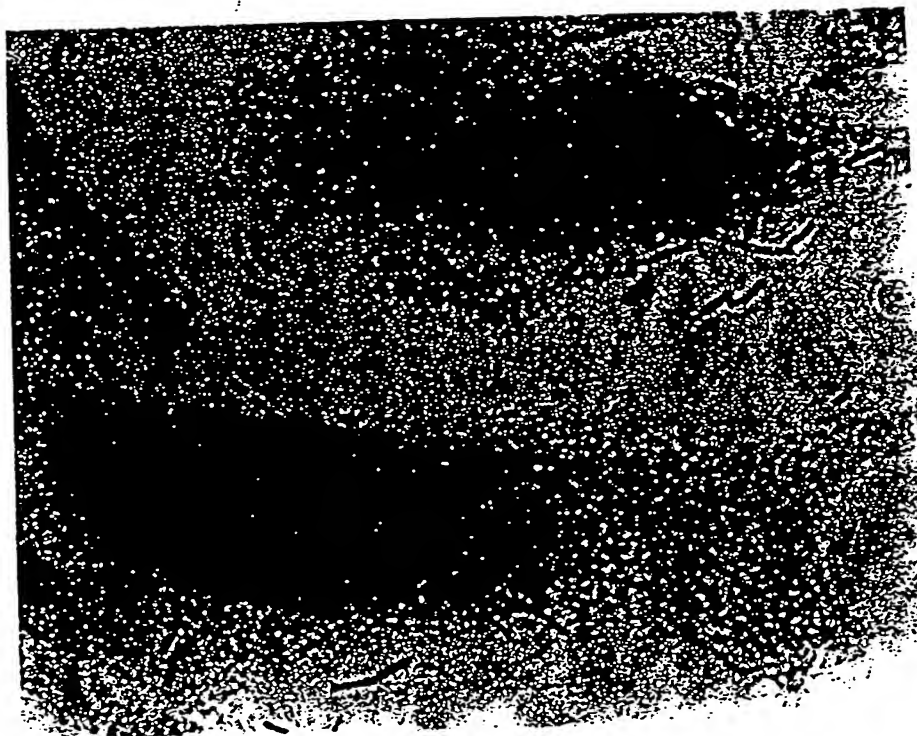


Fig. 1



A



B

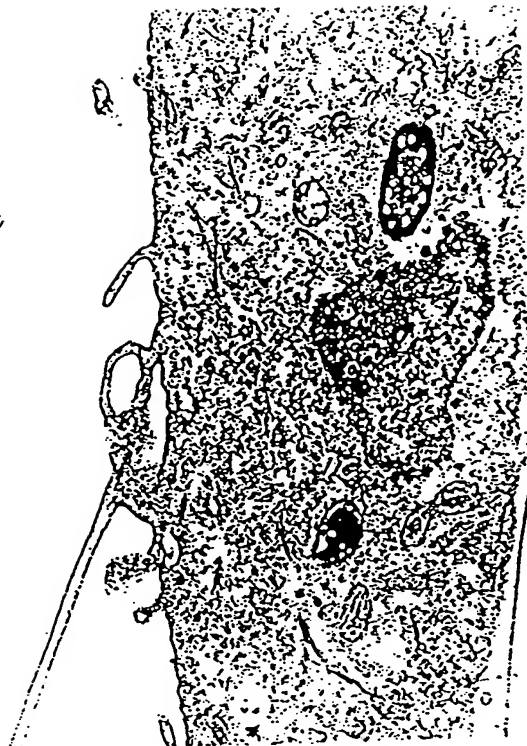
FIGURE 1

FIGURE 2

B



D



A



C

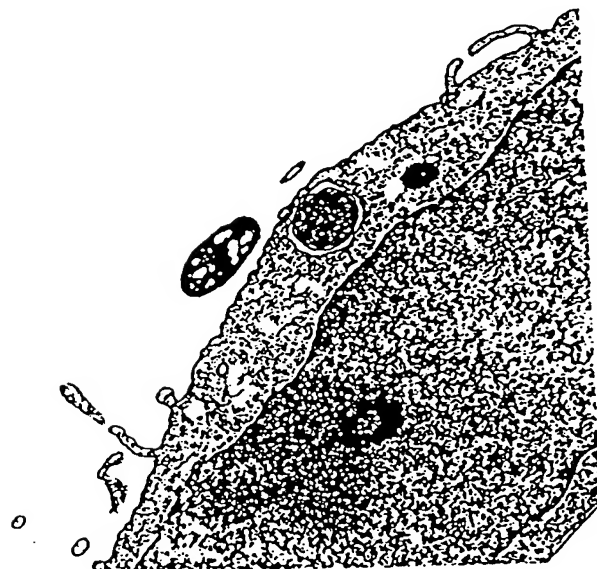


Fig. 3

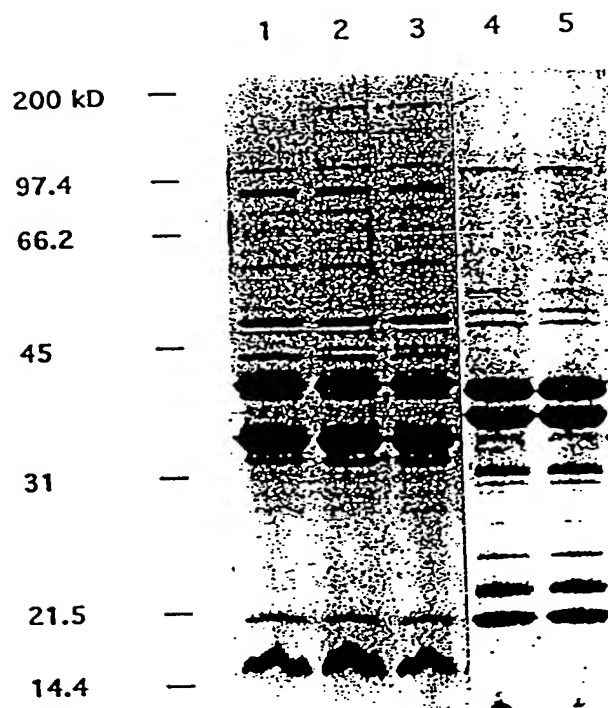


FIGURE 3

Fig. 4

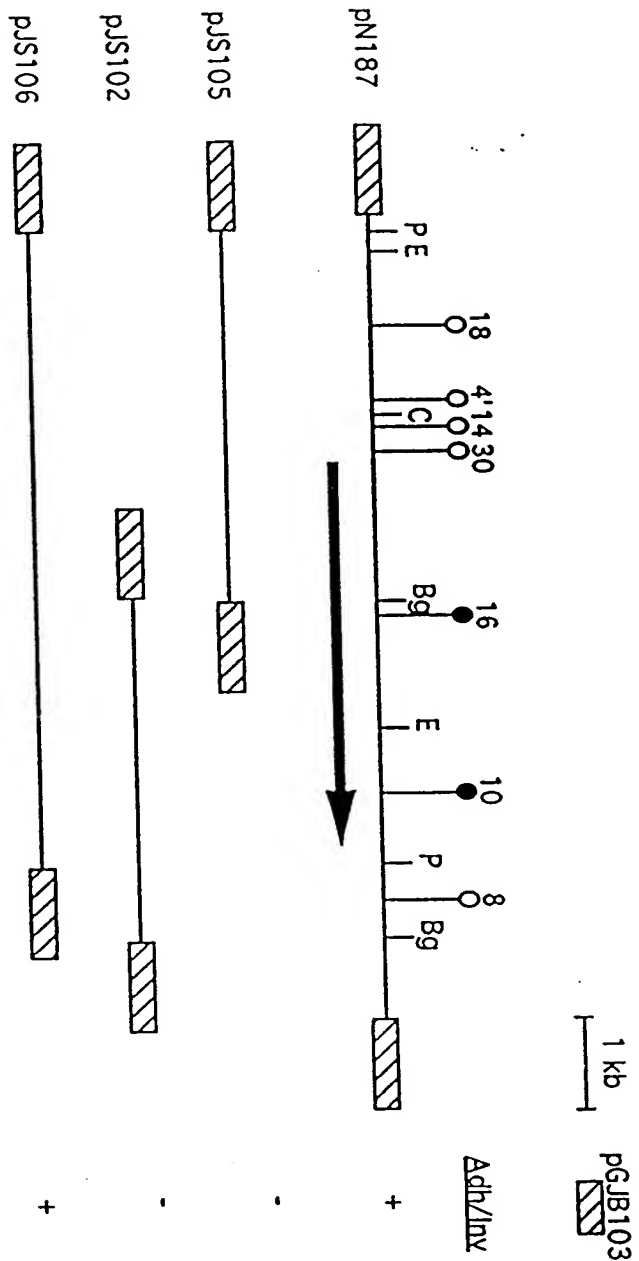
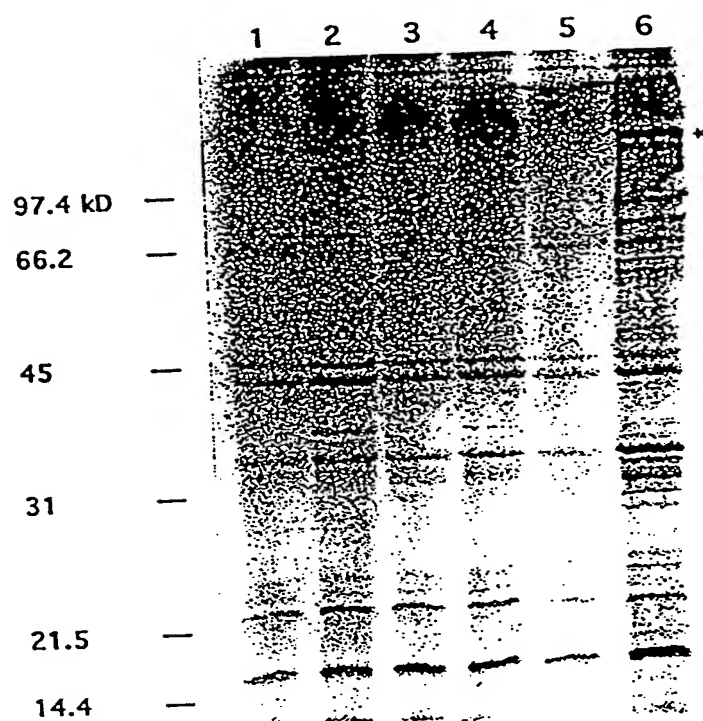


FIGURE 4

Fig. 5



— FIGURE 5 —

10 30 50 70 90  
 AATAGTCGTTAACTAGTATTTTTTAATACGAAAAATTACTTAATTAATAAACATTATGAAAAAACTGTATTCGTCTTAATTTT  
 -35 -10 M K K T V F R L N F  
 110 130 150 170  
 TAACCGCTTGCATTTTCATTAGGGATAGTATCGCAAGCGTGGGCTGGTCACACTTATTTTGGGATTGATTACCAATATTATCGTGATTTT  
 T A C I S L G I V S Q A W A G H T Y F G I D Y Q Y Y R D F  
 190 210 230 250 270  
 CCGAGAATAAAGGGAAGTTACAGTTGGGGCTCAAAATATTAAGGTTTATAACAAACAAGGGCAATTAGTTGGCACATCAATGACAAAA  
 E N K G K F T V G A Q N I K V Y N K Q G Q L V G T S M T K  
 290 310 330 350  
 CCCCgatgattgatttttctgtagtgtcacgtaacggcgtggcagccttggttgaaaatcaatatattgtgagcgtggcacataacgta  
 P M I D F S V S R N G V A A L V E N Q Y I V S V A H N V  
 370 390 410 430 450  
 GATATACAGATGTTGATTTTGGTGCAGAGGGAAACAACCCCGATCAACATCGTTTTACTTATAAGATTGTAAACGAAATAACTACAAA  
 Y T D V D F G A E G N N P D Q H R F T Y K I V K R N N Y K  
 470 490 510 530  
 AAGATAATTTACATCCTTATGAGGACGATTACCATAATCCACGATTACATAAATTCGTTACAGAAGCGGCTCCAATTGATATGACTTCG  
 D N L H P Y E D D Y H N P R L H K F V T E A A P I D M T S  
 550 570 590 610 630  
 ATATGAATGGCAGTACTTATTCAGATAGAACAATATCCAGAACGTGTTGTTATCGGCTCTGGACGGCAGTTTGGCGAAATGATCAA  
 M N G S T Y S D R T K Y P E R V R I G S G R Q F W R N D Q  
 650 670 690 710  
 ACAAAGGCGACCAAGTTGCCGGTGATATCATTATCTGACAGCTGGCAATACACACAATCAGCGTGGAGCAGGTAATGGATATTCGTAT  
 K G D Q V A G A Y H Y L T A G N T H N Q R G A G N G Y S Y...  
 730 750 770 790 810  
 TGGGAGGCGATGTTTCGTAAAGCGGGAGAATATGGTCCATTACCGATTGCAGGCTCAAAGGGGGACAGTGGTTCTCCGATGTTTATTTAT  
 G G D V R K A G E Y G P L P I A G S K G D S G S P M F I Y  
 830 850 870 890  
 ATGCTGAAAAACAAAATGGTTAATTAATGGGATATTACGGGAAGGCAACCTTTTGAAGGCAAAGAAAATGGGTTTCAATTGGTTCGC  
 A E K Q K W L I N G I L R E G N P F E G K E N G F Q L V R  
 910 930 950 970 990  
 AATCTTATTTTATGAAATTTTCGAAAGAGATTTACATACATCACTTTACACCCGAGCTGGTAATGGAGTGTACACAATTAGTGGAAT  
 C S Y F D E I F E R D L H T S L Y T R A G N G V Y T I S G N  
 1010 1030 1050 1070  
 GATAATGGTCAGGGGTCTATAACTCAGAAATCAGGAATACCATCAGAAATTAATAATACGTTAGCAAATATGAGTTTACCTTTGAAAGAG  
 D N G Q G S I T Q K S G I P S E I K I T L A N M S L P L K E  
 1090 1110 1130 1150 1170  
 AAGGATAAAGTTTATAATCCTAGATATGACGGACCTAATATTTATTTCTCCACGTTTAAACAATGGAGAAACGCTATATTTTATGGATCAA  
 K D K V H N P R Y D G P N I Y S P R L N N G E T L Y F M D Q  
 1190 1210 1230 1250  
 AAACAAGGATCATTAATCTTCGATCTGACATTAACCAAGGGGCGGGTGGTCTTTATTTTGGAGGTAATTTTACAGTATCTCCAAATTCT  
 K Q G S L I F A S D I N Q G A G G L Y F E G N F T V S P N S  
 1270 1290 1310 1330 1350  
 AACCAAACTTGGCAAGGAGCTGGCATAATGTAAGTGAAGTAAAGTAAATGGCGTGGAAACATGATCGACTTTCT  
 N Q T W Q G A G I H V S E N S T V T W K V N G V E H D R L S  
 1370 1390 1410 1430  
 AAAATTGGTAAAGGAACATTGCACGTTCAAGCCAAAGGGGAAAAATAAAGGTTTCGATCAGCGTAGGCGATGGTAAAGTCATTTTGGAGCAG  
 K I G K G T L H V Q A K G E N K G S I S V G D G K V I L E Q

FIGURE 6A

1450 1470 1490 1510 1530  
 AGGCAGACGATCAAGGCAACAAACAAGCCTTTAGTGAAATTGGCTTGGTTAGCGGCAGAGGGACTGTTCAATTAACGATGATAAACAA  
 A D D Q G N K Q A F S E I G L V S G R G T V Q L N D D K Q

1550 1570 1590 1610  
 TTGATACCGATAAATTTTATTTTCGGCTTTCTGTTGGTTCGCTTAGATCTTAACGGGCATTATTAACCTTTAAACGTATCCAAAATACG  
 D T D K F Y F G F R G G R L D L N G H S L T F K R I Q N T

1630 1650 1670 1690 1710  
 ACGAGGGGGCAATGATTGTGAACCATAATACTCAAGCCGCTAATGTCACTATTACTGGGAACGAAAGCATTGTTGTACCTAATGGA  
 E G A M I V N H N T T Q A A N V T I T G N E S I V L P N G

1730 1750 1770 1790  
 ATAATATTAATAAACTTGATTACAGAAAAGAAATTGCCTACAACGGTTGGTTTGGCGAAACAGATAAAAAATAACACAATGGGCGATTA  
 N I N K L D Y R K E I A Y N G W F G E T D K N K H N G R L

1810 1830 1850 1870 1890  
 ACCTTATTTATAAACCAACCACAGAAGATCGTACTTTGCTACTTTTCAGGTGGTACAAATTTAAAGGCGATATTACCCAAACAAAGGT  
 L I Y K P T T E D R T L L L S G G T N L K G D I T Q T K G

1910 1930 1950 1970  
 AACTATTTTTTCAGCGGTAGACCGACACCGCACGCCTACAATCATTTAAATAAACGTTGGTCAGAAATGGAAGGTATACCACAAGGCGAA  
 L F F S G R P T P H A Y N H L N K R W S E M E G I P Q G E

1990 2010 2030 2050 2070  
 TTGTGTGGGATCACGATTGGATCAACCGTACATTTAAAGCTGAAAACCTTCCAAATTAAGGCGGAAGTGCGGTGGTTTCTCGCAATGTT  
 V W D H D W I N R T F K A E N F Q I K G G S A V V S R N V

2090 2110 2130 2150  
 CTTCAATTGAGGGAAATTGGACAGTCAGCAATAATGCAAATGCCACATTTGGTGTGGTCCAAATCAACAAAATACCATTGTCACGCGT  
 S I E G N W T V S N N A N A T F G V V P N Q Q N T I C T R

2170 2190 2210 2230 2250  
 CAGATTGGACAGGATTAACGACTTGTCAAAAAGTGGATTTAACCGATACAAAAGTTATTAATTCTATACCAAAAACACAAATCAATGGC  
 D W T G L T T C Q K V D L T D T K V I N S I P K T Q I N G

2270 2290 2310 2330  
 CTATTAATTTAACTGATAATGCAACGGCGAATGTTAAAGGTTTAGCAAACTTAATGGCAATGTCACTTTAACAAATCACAGCCAATTT  
 S I N L T D N A T A N V K G L A K L N G N V T L T N H S Q F

2350 2370 2390 2410 2430  
 ACATTAAGCAACAATGCCACCCAAATAGGCAATATTCGACTTTCCGACAATTCAACTGCAACGGTGGATAATGCAAACCTGAACGGTAAT  
 L S N N A T Q I G N I R L S D N S T A T V D N A N L N G N

2450 2470 2490 2510  
 GTGCATTTAACGGATTACGCTCAATTTTCTTTAAAAACAGCCATTTTTCGCACCAAATTCAGGGAGACAAAGGCACAACAGTGACGTTG  
 V H L T D S A Q F S L K N S H F S H Q I Q G D K G T T V T L

2530 2550 2570 2590 2610  
 GAAAATGCGACTTGGACAATGCCTAGCGATACTACATTGCAGAATTTAACGCTAAATAACAGTACGATCACGTTAAATTCAGCTTATTCA  
 E N A T W T M P S D T T L Q N L T L N N S T I T L N S A Y S

2630 2650 2670 2690  
 GCTAGCTCAAACAATACGCCACGTGCGCCGTTATTAGAGACGGAAACAACGCCAACATCGGCAGAACATCGTTTCAACACATTGACAGTA  
 A S S N N T P R R R S L E T E T T P T S A E H R F N T L T V

2710 2730 2750 2770 2790  
 AATGGTAAATTGAGTGGGCAAGGCACATTCCAATTTACTTCATCTTTATTTGGCTATAAAAGCGATAAATTAATTAATCAATGACGCT  
 N G K L S G Q G T F Q F T S S L F G Y K S D K L K L S N D A

2810 2830 2850 2870  
 GAGGGCGATTACATATTATCTGTTGCAACACAGGCAAAGAACC CGAAACCTTGAGCAATTAACCTTTGGTTGAAAGCAAAGATAATCAA  
 E G D Y I L S V R N T G K E P E T L E Q L T L V E S K D N Q

FIGURE 6B

2890 2910 2930 2950 2970  
 CCGTTATCAGATAAGCTCAAATTTACTTTAGAAAATGACCACGTTGATGCAGGTGCATTACGTTATAAATTAGTGAAGAATGATGGCGAA  
 P L S D K L K F T L E N D H V D A G A L R Y K L V K N D G E

2990 3010 3030 3050  
 TTCCGCTTGCATAACCCAATAAAAGAGCAGGAATTGCACAATGATTAGTAAGAGCAGAGCAAGCAGAACGAACATTAGAAGCCAAACAA  
 F R L H N P I K E Q E L H N D L V R A E Q A E R T L E A K Q

3070 3090 3110 3130 3150  
 GTTGAACCGACTGCTAAACACAAACAGGTGAGCCAAAAGTGCGGTCAAGAAGAGCAGCGAGAGCAGCGTTTCTGATACCCTGCCTGAT  
 V E P T A K T Q T G E P K V R S R R A A R A A F P D T L P D

3170 3190 3210 3230  
 CAAAGCCTGTAAACGCATTAGAAGCCAAACAAAGCTGAACTGACTGCTGAAACACAAAAAAGTAAGGCAAAAAACAAAAAAGTGCGGTCA  
 Q S L L N A L E A K Q A E L T A E T Q K S K A K T K K V R S

3250 3270 3290 3310 3330  
 AAAAGAGCAGTGTTTTCTGATCCCCTGCTTGATCAAAGCCTGTTGCGATTAGAAGCCGCACTTGAGGTTATTGATGCCCCACAGCAATCG  
 K R A V F S D P L L D Q S L F A L E A A L E V I D A P Q Q S

3350 3370 3390 3410  
 GAAAAAGATCGTCTAGCTCAAGAAGAAGCGGAAAAACAACGCAACAAAAAGACTTGATCAGCCGTTATTCAAATAGTGC GTTATCAGAA  
 E K D R L A Q E E A E K Q R K Q K D L I S R Y S N S A L S E

3430 3450 3470 3490 3510  
 TTATCTGCAACAGTAAATAGTATGCTTTCTGTTCAAGATGAATTAGATCGTCTTTTGTAGATCAAGCACAATCTGCCGTGTGGACAAAT  
 L S A T V N S M L S V Q D E L D R L F V D Q A Q S A V W T N

3530 3550 3570 3590  
 ATCGCACAGGATAAAAAGACGCTATGATTCTGATGCGTTCCGTGCTTATCAGCAGCAGAAAAACGAACTTACGTCAAATTGGGGTGCAAAAA  
 I A Q D K R R Y D S D A F R A Y Q Q Q K T N L R Q I G V Q K

3610 3630 3650 3670 3690  
 GCCTTAGCTAATGGACGAATTGGGGCAGTTTTCTCGCATAGCCGTTGAGATAATACCTTTGATGAACAGGTTAAAAATCACGCGAATTAA  
 A L A N G R I G A V F S H S R S D N T F D E Q V K N H A T L

3710 3730 3750 3770  
 ACGATGATGTCGGGTTTTGCCCAATATCAATGGGGCGATTTACAATTTGGTGTAACGTGGGAACGGGAATCAGTGCGAGTAAATGGCT  
 T M M S G F A Q Y Q W G D L Q F G V N V G T G I S A S K M A

3790 3810 3830 3850 3870  
 GAAGAACAAAGCCGAAAAATTATCGAAAAAGCGATAAATTATGGCGTGAATGCAAGTTATCAGTTCCGTTTAGGGCAATTGGGCATTGAG  
 E E Q S R K I H R K A I N Y G V N A S Y Q F R L G Q L G I Q

3890 3910 3930 3950  
 CCTTATTTTGGAGTTAATCGCTATTTTATTGAACGTGAAAATTATCAATCTGAGGAAGTGAGAGTGAAAAACGCCTAGCCTTGCAATTAAT  
 P Y F G V N R Y F I E R E N Y Q S E E V R V K T P S L A F N

3970 3990 4010 4030 4050  
 CGCTATAATGCTGGCATTGAGTTGATTATACATTTACTCCGACAGATAATATCAGCGTTAAGCCTTATTTCTTCGTCAATTATGTTGAT  
 R Y N A G I R V D Y T F T P T D N I S V K P Y F F V N Y V D

4070 4090 4110 4130  
 GTTTCAAACGCTAACGTACAAACACGGTAAATCTCACGGTGTGCAACAACCATTTGGACGTTATTGGCAAAAAGAAGTGGGATTAAAG  
 V S N A N V Q T T V N L T V L Q Q P F G R Y W Q K E V G L K

4150 4170 4190 4210 4230  
 GCAGAAATTTTACATTTCCAAATTTCCGCTTTTATCTCAAATCTCAAGGTTTCAAACTCGGCAAAACAGCAAAATGTGGGCGTGAAATTG  
 A E I L H F Q I S A F I S K S Q G S Q L G K Q Q N V G V K L

4250 4270 4290 4310  
 GGCTATCGTTGGTAAAAATCAACATAATTTTATCGTTTATTGATAACAAGGTGGGTGAGATCAGATCCCACCTTTTTTATTCCAATAAT  
 G Y R W \*


—  —

FIGURE 6C



Fig. 2

	1					50
Hap	MKKTIVFRLNF	LTACISLGIV	SQAWAGHTYF	GIDYQYYRDF	AENKKGKFTVG	
HK368IGA	MLNKKFKLNF	IALTVAYALT	PYTEAALVRD	DVDYQIFRDF	AENKKGKFSVG	
HK393IGA	MLNKKFKLNF	IALTVAYALT	PYTEAALVRD	DVDYQIFRDF	AENKKGKFSVG	
HK715IGA	MLNKKFKLNF	IALTVAYALT	PYTEAALVRD	DVDYQIFRDF	AENKGRFSVG	
HK61IGA	MLNKKFKLNF	IALTVAYALT	PYTEAALVRD	DVDYQIFRDF	AENKKGKFSVG	
Consensus	M----F-LNF	-----	----A-----	--DYQ--RDF	AENKKG-F-VG	
	51					100
Hap	AQNIKVYNKQ	GQLVGTSMTK	A.PMIDFSV	SRNG.VAALV	ENQYIVSVAH	
HK368IGA	ATNVLVKDKN	NKDLGTALPN	GIPMIDFSV	DVDKRIATLI	NPQYVVGVKH	
HK393IGA	ATNVEVRDKN	NRLGNVLPN	GIPMIDFSV	DVDKRIATLV	NPQYVVGVKH	
HK715IGA	ATNVEVRDKN	NHSLGNVLPN	GIPMIDFSV	DVDKRIATLI	NPQYVVGVKH	
HK61IGA	ATNVEVRDKK	NQSLGSALPN	GIPMIDFSV	DVDKRIATLV	NPQYVVGVKH	
Consensus	A-N--V--K-	----G-----	--PMIDFSV	-----A-L-	--QY-V-V-H	
	101					150
Hap	.....NVGY	TDVDFGAEGN	NPQDHR....	..FTYKIVKR	NNY.....	
HK368IGA	VSNGVSELHF	GNLNGNMNG	NAKAHROVSS	EENRYFSVEK	NEYPTKLNGK	
HK393IGA	VSNGVSELHF	GNLNGNMNG	NAKAHROVSS	EENRYYTVEK	NEYPTKLNGK	
HK715IGA	VSNGVSELHF	GNLNGNMNG	NDKSHROVSS	EENRYFSVEK	NEYPTKLNGK	
HK61IGA	VSNGVSELHF	GNLNGNMNG	NAKSHROVSS	EENRYYTVEK	NNFPTENVTS	
Consensus	-----	-----	N---HR----	----Y--V--	N-----	
	151					200
Hap	....KKDNLH	PYEDDYHNPR	LHKEVTEAAP	IDM.TSNMNG	STYSDRTKYP	
HK368IGA	TVTTEQ.TQ	KRREDYYMPR	LDKEVTEVAP	IEASTASSDA	GTYNQNKYP	
HK393IGA	AVTTEDQ.AQ	KRREDYYMPR	LDKEVTEVAP	IEASTDSSTA	GTYNKDKYP	
HK715IGA	AVTTEDQ.TQ	KRREDYYMPR	LDKEVTEVAP	IEASTASSDA	GTYNQNKYP	
HK61IGA	FTTKEEQDAQ	KRREDYYMPR	LDKEVTEVAP	IEASTANNK	GEYNNSDKYP	
Consensus	-----	----DY--PR	L-KEVTE-AP	I---T-----	--Y----KYP	
	201					250
Hap	ERVRIQSGRQ	F.....	.....WRNDQ	DKGDQVAGAY		
HK368IGA	AFVRLGSGSQ	FIYKKGDNYS	LIL.....N	NH....EVGG	NNLKLVGDAY	
HK393IGA	YFVRLGSGTQ	FIYENGTRYE	LWL.....G	KEGQKSDAGG	YNLKLVGDAY	
HK715IGA	AFVRLGSGSQ	FIYKKGDNYS	LIL.....N	NH....EVGG	NNLKLVGDAY	
HK61IGA	AFVRLGSGSQ	FIYKKGSRQ	LILTEKDKQG	NLLRNWDVGG	DNLELVGNAY	
Consensus	--VR-GSG-Q	F-----	-----	-----	-----V--AY	

—  —  
FIGURE 7A

	251				300
Hap	HYLTAGNTHN	QRGAGNGYSY	LGG.....D	VRKAGEYGPL	PIAGSKGDSG
HK368IGA	TYGLAGTPYK	VNHENGLIG	FGNSKEEHS	PKGILSQDPL	TNYAVLGDSG
HK393IGA	TYGLAGTPYE	VNHENDGLIG	FGNSNNEYIN	PKEILSKKPL	TNYAVLGDSG
HK715IGA	TYGLAGTPYK	VNHENGLIG	FGNSKEEHS	PKGILSQDPL	TNYAVLGDSG
HK61IGA	TYGLAGTPYK	VNHENGLIG	FGNSKEEHS	PKGILSQDPL	TNYAVLGDSG
Consensus	-Y--AG----	-----G---	-G-----	-----PL	-----GDSG
					*
	301				350
Hap	SPMFIYDAEK	QKWLINGILR	EGNPFEGKEN	GFQLVRKSYF	D.EIFERDLH
HK368IGA	SPLFVYDREK	GKWLFILGSYD	FWAGYN....	.....KKSQ	EWNIYKSQFT
HK393IGA	SPLFVYDREK	GKWLFILGSYD	YWAGYN....	.....KKSQ	EWNIYKPEFA
HK715IGA	SPLFVYDREK	GKWLFILGSYD	FWAGYN....	.....KKSQ	EWNIYKPEFA
HK61IGA	SPLFVYDREK	GKWLFILGSYD	FWAGYN....	.....KKSQ	EWNIYKHEFA
Consensus	SP-F-YD-EK	-KWL--G---	-----	-----KS--	---I-----
	351				400
Hap	TSLYTRAGNG	VYTISGNDNG	QGSITQKSGI	PSEIKITLAN	MSLPIKEKDK
HK368IGA	KDVLNKDSAG	SLIGSKIDYS	WSSNGKTSTI	TGGEK....S	INVDLAD...
HK393IGA	EKIYEQYSAG	SLIGSKIDYS	WSSNGKTSTI	TGGEK....S	INVDLAD...
HK715IGA	KTVLDKDTAG	SLTGSNTQYN	WNPTGKTSVI	SNGSE....S	INVDLFD...
HK61IGA	EKIYQQYSAG	SLTGSNTQYT	WQATGSTSTI	TGGGE....P	LSVDLTD...
Consensus	-----G	----S-----	-----S-I	-----	----L-----
	401				450
Hap	VHNPRYDGN	IYSPRLNNGE	TLYFMDQKQG	SLIFASDINQ	GAGGLYFEGN
HK368IGA	.....GKD.	....KPNHGK	SVTFEG..SG	TLTLNNNIDQ	GAGGLFFEGD
HK393IGA	.....GKD.	....KPNHGK	SVTFEG..SG	TLTLNNNIDQ	GAGGLFFEGD
HK715IGA	.....SSQD	TDSKKNNHGK	SVTLRG..SG	TLTLNNNIDQ	GAGGLFFEGD
HK61IGA	.....GKD.	....KPNHGK	SITLKG..SG	TLTLNNHIDQ	GAGGLFFEGD
Consensus	-----	-----N-G-	-----G	-L-----I-Q	GAGGL-FEG-
	451				500
Hap	FTVSPNSNQ.	TWQGAGIHVS	ENSTVIWKVN	GVEHDRLSKI	GKGTILHVQAK
HK368IGA	YEVKGTSDNT	TWKGAGVSVA	EGKTVIWKVH	NPQYDRLAKI	GKGTILIVEGT
HK393IGA	YEVKGTSDNT	TWKGAGVSVA	EGKTVIWKVH	NPQYDRLAKI	GKGTILIVEGT
HK715IGA	YEVKGTSDST	TWKGAGVSVA	DGKTVIWKVH	NPKSDRLAKI	GKGTILIVEGK
HK61IGA	YEVKGTSDST	TWKGAGVSVA	DGKTVIWKVH	NPKYDRLAKI	GKGTILVVEGK
Consensus	--V---S---	TW-GAG--V-	---TVIWKV-	----DRL-KI	GKGTIL-V---


—  —

FIGURE 7B

	501		550
Hap	GENKGSISVG	DGKVILEQQA	DDQGNKQAFS EIGLVSGRGT VQLNDDKQFD
HK368IGA	GDNKGSILKVG	DGTVILKQQT	NGSGQ.HAFA SVGIVSGRST LVLNDDKQVD
HK393IGA	GDNKGSILKVG	DGTVILKQQT	NGSGQ.HAFA SVGIVSGRST LVLNDDKQVD
HK715IGA	GENKGSILKVG	DGTVILKQQA	DANNKVAFS QVGIVSGRST VVLNDDKQVD
HK61IGA	GKNEGLKVG	DGTVILKQKA	DANNKVQAFS QVGIVSGRST LVLNDDKQVD
Consensus	G-N-G---VG	DG-VIL-Q--	-----AF- --G-VSGR-T---LNDDKQ-D
	551		600
Hap	TDKIFYGFRG	GRDLINGHSL	TFKRIQNIDE GAMIVNHNT QAANVTITGN
HK368IGA	PNSIYFGRG	GRDLINGNSL	TFDHIRNIDD GARLVNHMT NASNITITGE
HK393IGA	PNSIYFGRG	GRDLINGNSL	TFDHIRNIDE GARLVNHSTS KHSTVTITGD
HK715IGA	PNSIYFGRG	GRLDANGNL	TFEHIRNIDD GARLVNHNTS KTSTVTITGE
HK61IGA	PNSIYFGRG	GRDLINGNSL	TFDHIRNIDD GARVVNHMT NTSNITITGE
Consensus	----YFGRG	GRLD-NG--L	TF--I-N-D- GA--VNH--- ----TITG-
	601		650
Hap	ESIVLPNG..	.....	.....
HK368IGA	SLITDPNTIT	PYNIDAPDED	NPYAFRIKD GGQLYLNLEN YTTYALRKGA
HK393IGA	NLITDPNNVS	IYYVKPLEDD	NPYAIRQIKY GYQLYFNEEN RTYYALKKDA
HK715IGA	SLITDPNTIT	PYNIDAPDED	NPYAFRIKD GGQLYLNLEN YTTYALRKGA
HK61IGA	SLITDPNTIT	SYNIEAQDD	HPLRIRSIPY R.QLYFNQDN RSYTYLKKGA
Consensus	--I--PN---	-----	-----
	651		700
Hap	.....	.....	.....N NINKLDYRKE IAYNGWFGET
HK368IGA	STRSELPKNS	GESNENWLYM	GKTSDEAKRN VMNHINNERM NGNGYFGEE
HK393IGA	SIRSEFPQNR	GESNNSWLYM	GTEKADAQKN AMNHINNERM NGNGYFGEE
HK715IGA	STRSELPKNS	GESNENWLYM	GKTSDEAKRN VMNHINNERM NGNGYFGEE
HK61IGA	STRSELPQNS	GESNENWLYM	GRTSDEAKRN VMNHINNERM NGNGYFGEE
Consensus	-----	-----	-----N --N----- ---NG-FGE-
	701		750
Hap	D.KNKHNGRL	NLIYKPTTED	RTLLLSGGTN LKGDITQTKG KLFFSGRPTP
HK368IGA	EGK..NNGNL	NVTFKGKSEQ	NRFLLTGGTN LNGDLTVEKG TLFLSGRPTP
HK393IGA	EGK..NNGNL	NVTFKGKSEQ	NRFLLTGGTN LNGDLNVQQG TLFLSGRPTP
HK715IGA	EGK..NNGNL	NVTFKGKSEQ	NRFLLTGGTN LNGDLKVEKG TLFLSGRPTP
HK61IGA	ETKATQNGKL	NVTFNGKSDQ	NRFLLTGGTN LNGDLNVEKG TLFLSGRPTP
Consensus	--K---NG-L N-----	---	LL-GGTN L-GD-----G -LF-SGRPTP


—  —

FIGURE 7C

	751		800
Hap	HAYNHLNKRW	SEMEG..IPQ	GEIVWDHDI NRTFKAENFQ IKGGSVVVS.
HK368IGA	HARDIAGISS	TKKDPHFAEN	NEVVVEDDWI NRNEKATTMN VTGNASLYSG
HK393IGA	HARDIAGISS	TKKDSHFSEN	NEVVVEDDWI NRNEKATTMN VTNNATLYSG
HK715IGA	HARDIAGISS	TKKDQHEAEN	NEVVVEDDWI NRNEKATTMN VTNNATLYSG
HK61IGA	HARDIAGISS	TKKDPHFTEN	NEVVVEDDWI NRNEKATTMN VTGNASLYSG
Consensus	HA-----	-----	-E-V---DWI NR-EKA-----S-
	801		850
Hap	RNVSSIEGNW	TVSNANATF	GVVFNQNTI CTRSDWTGLT TCQKVDLIDT
HK368IGA	RNVANITSNI	TASNKAQVHI	GY..KTGDTV CVRSDYTGIV TCTIDKLS.
HK393IGA	RNVESITSNI	TASNNAKVHI	GY..KAGDTV CVRSDYTGIV TCTIDKLS.
HK715IGA	RNVANITSNI	TASNAKVHI	GY..KAGDTV CVRSDYTGIV TCTIDKLS.
HK61IGA	RNVANITSNI	TASNKAQVHI	GY..KTGDTV CVRSDYTGIV TCHNSNLSE.
Consensus	RNV--I--N-	T-S--A----	G-----T- C-RSD-TG-- TC----L----
	851		900
Hap	KVINSIPKTQ	INGSINLTDN	ATANVKGLAK LNGNVTLTNH SQFTLSNNAT
HK368IGA	KALNSFNPTN	LRGNVNLTES	A.....
HK393IGA	KALNSFNPTN	LRGNVNLTES	A.....
HK715IGA	KALNSFNATN	VSGNVNLSEN	A.....
HK61IGA	KALNSFNPTN	LRGNVNLTEN	A.....
Consensus	K--NS---T-	--G--NL---	A-----
	901		950
Hap	QIGNIRLSDN	STATVDNANL	NGNVHLIDSA QFSLKNSHFS HQIQGDKGTT
HK368IGA	.....	.NEVLGKANL	FGTIQSRGNS QVRLT.....
HK393IGA	.....	.NEVLGKANL	FGTIQSRGNS QVRLT.....
HK715IGA	.....	.NEVLGKANL	FGTISGTGNS QVRLT.....
HK61IGA	.....	.SFTLGKANL	FGTIQSIGTS QVNLK.....
Consensus	-----	-----ANL	-G----- Q--L-----
	951		1000
Hap	VTLENATWIM	PSDTTLQNL	LNNSTITLNS AYSASSNNTN RRRSLETETT
HK368IGA	...ENSHWHL	TGNSDVHOLD	LANGHIHLNS ADNSNNVTK. ....
HK393IGA	...ENSHWHL	TGNSDVHOLD	LANGHIHLNS ADNSNNVTK. ....
HK715IGA	...ENSHWHL	TGNSNVNQLN	LDKGHIHLNA QNDANKVTT. ....
HK61IGA	...ENSHWHL	TGNSNVNQLN	LTNGHIHLNA QNDANKVTT. ....
Consensus	---EN--W--	-----L-	L----I-LN-

FIGURE 7D

	1001		1050
Hap	PTSAEHRFNT	LTVNGKLSGQ	GTFQFTSSLF GYKSDKLKLS NDAEGDYILS
HK368IGA	.....YNT	LTVNS.LSGN	GSFYLLTDLS NKQGDVWVT KSATGNFTLQ
HK393IGA	.....YNT	LTVNS.LSGN	GSFYLLTDLS NKQGDVWVT KSATGNFTLQ
HK715IGA	.....YNT	LTVNS.LSGN	GSFYLLTDLS NKQGDVWVT KSATGNFTLQ
HK61IGA	.....YNT	LTVNS.LSGN	GSFYVWVFT NNKSNKVVVN KSATGNFTLQ
Consensus	-----NT	LTVN--LSG-	G-F----- --K---- --A-G--L-
	1051		1100
Hap	VRNTGKEPET	LEQLTLVESK	DNQPLSDKLK FTLENDHVDA GALRYKLVKN
HK368IGA	VADKTGEPNH	.NELTLEFAS	KAQR..DHLN VSLVGNTVDL GAWKYKLRNV
HK393IGA	VADKTGEPNH	.NELTLEFAS	KAQR..DHLN VSLVGNTVDL GAWKYKLRNV
HK715IGA	VADKTGEPTK	.NELTLEFAS	NATR..NNLN VSLVGNTVDL GAWKYKLRNV
HK61IGA	VADKTGEPNH	.NELTLEFAS	NATR..NNLE VTLANGSVDR GAWKYKLRNV
Consensus	V-----EP--	---LTL---	-----L- --L----VD- GA--YKL---
	1101		1150
Hap	DGEFRLHNPI	KEQELHNDLV	.....
HK368IGA	NGRYDLYNP.	.EVEKRNQTV	DTTNITTPNN IQADVPSVPS NNEEIARVDE
HK393IGA	NGRYDLYNP.	.EVEKRNQTV	DTTNITTPNN IQADVPSVPS NNEEIARVDE
HK715IGA	NGRYDLYNP.	.EVEKRNQTV	DTTNITTPNN IQADVPSVPS NNEEIARV.E
HK61IGA	NGRYDLYNP.	.EVEKRNQTV	DTTNITTPND IQADAPSAQS NNEEIARV.E
Consensus	-G---L-NP-	-E-E--N--V	-----
	1151		1200
Hap	.....	.....	.....
HK368IGA	APVPPPAPAT	.....	.....
HK393IGA	APVPPPAPAT	.....	.....
HK715IGA	TPVPPPAPAT	.....	.....
HK61IGA	TPVPPPAPAT	ESALASEQPE	TRPAETAQPA MEETNTANST ETAPKSDTAT
Consensus	-----	-----	-----
	1201		1250
Hap	.....	.....	RAEQAERTLE AKQVEPT...
HK368IGA	.....	PSETTETVAE	NSKQESKTVE KNEQDATETT AQNREVAKA
HK393IGA	.....	PSETTETVAE	NSKQESKTVE KNEQDATETT AQNREVAKA
HK715IGA	.....	PSETTETVAE	NSKQESKTVE KNEQDATETT AONGEVAEEA
HK61IGA	QTENPNSES	PSETTEKVAE	NPPQENETVA KNEQEATEPT PQNGEVAKED
Consensus	-----	-----	---Q---T-- -----T---


—  —

FIGURE 7E

	1251		1300
Hap	.....AKTQT GE.....	.....	.....
HK368IGA	KSNVKANTQT NEVAQSGSET KETQTTETK.	.....	ETATVE
HK393IGA	KSNVKANTQT NEVAQSGSET KETQTTETK.	.....	ETATVE
HK715IGA	KPSVKANTQT NEVAQSGSET EETQTTETK.	.....	ETAKVE
HK61IGA	QPTVEANTQT NEATQSEGKT EETQTAETKS	EPTESVTVSE	NQPEKTVSQS
Consensus	-----A-TQT -E-----	-----	-----
	1301		1350
Hap	.....	.....	.....
HK368IGA	KEEK.....	.....	.....
HK393IGA	KEEK.....	.....	.....
HK715IGA	KEEKAKVEKE EKAKVEKDEI	QEAPQMASET	SPKQAKPAPK EVSIDIKVEE
HK61IGA	TEDKVVVEKE EKAKVETEET	QKAPQVTSKE	PPKQAEPAPE EVPTDINAEE
Consensus	-----	-----	-----
	1351		1400
Hap	.....	.....	.....
HK368IGA	.....	.....	.....
HK393IGA	.....	.....	.....
HK715IGA	TQVQAQPTQ STTVAAAEAT	SPNSKPAEET	.QPSEKTNAE PVTPVVSQKQ
HK61IGA	A..QALQQTQ PTTVAAAEET	SPNSKPAEET	QQPSEKTNAE PVTPVVS...
Consensus	-----	-----	-----
	1401		1450
Hap	.....	.....PKVRS	RRAARAAFPD TLP.....
HK368IGA	.....	AKVETE	KTOEVPKVTs QVSPKQEQSE T.....
HK393IGA	.....	AKVETE	KTOEVPKVTs QVSPKQEQSE T.....
HK715IGA	TENTTDQPTe	REKIAKVETE	KTOEPPQVAS QASPKQEQSE T.....
HK61IGA	.ENTATQPTe	TEETAKVEKE	KTOEVPQVAS QESPKQEQPA AKPOAQTKPQ
Consensus	-----	-----	-----P-V-S-----
	1451		1500
Hap	.....	.....	.....V
HK368IGA	.....	.....	.....V
HK393IGA	.....	.....	.....V
HK715IGA	.....	.....	.....V
HK61IGA	AEPARENVLt	TKNVGEPQPO	AQPQTQSTAV PTTGETAANS KPAAKPQAQA
Consensus	-----	-----	-----

FIGURE 7F

	1501		1550
Hap	.....D QSLNNALEA. ....KQAE	TAETQKSKAK	TKK.....
HK368IGA	QPQAEPAEN DPTVNIKEP. ....QSQTNT	TADTEQPAKE	TSSNVE....
HK393IGA	QPQAEPAEN DPTVNIKEP. ....QSQTNT	TADTEQPAKE	TSSNVE....
HK715IGA	QPQAVLESEN VPTVNNAEEV QAQLQTQTS	TVSTKQPAPE	NSINTG....
HK61IGA	KPQTEPAEN VSTVNTKEP. ....QSQTSA	TVSTEQPAKE	TSSNVEQPAP
Consensus	-----N-E-----Q-T-T-----		
	1551		1600
Hap	.....V RSKRAVSDP	LLDQSL....	
HK368IGA	.....QPV	ESTTVNTGNS	VVEN.....
HK393IGA	.....QPV	ESTTVNTGNS	VVEN.....
HK715IGA	.....SAT AITETAEKSD KPQTETAAST	EDASQHKANT	VADNSVANNS
HK61IGA	ENSINTGSAT TMTETAEKSD KPQMET..VT	ENDROPEANT	VADNSVANNS
Consensus	-----	-----	-----
	1601		1650
Hap	.....F ALEAALEVID APQOSEKDRL	AQEEAEKQRK	
HK368IGA	.....PENTTPATTQ	PTVNSESSN. .KPK.NRHR	
HK393IGA	.....PENTTPATTQ	PTVNSESSN. .KPK.NRHR	
HK715IGA	ESSEPKSRRR RSISQPOETS AEETTAASTD	ETTIADNSKR	SKPN.RRSRR
HK61IGA	ESSEKSRRR RSVSQPKETS AEETTASTQ	ETTVDNSVST	PKPRSRRTRR
Consensus	-----	-----	-----R-
	1651		1700
Hap	.....OKDLI	SRYSNSALSE	
HK368IGA	SVRSVPHNVE PATTSSND..	RSTVALCDLT	STNTNAVLS
HK393IGA	SVRSVPHNVE PATTSSND..	RSTVALCDLT	STNTNAVLS
HK715IGA	SVRS.....E PTVINGSD..	RSTVALRDLT	STNTNAVIS
HK61IGA	SVQINSYEPV ELPTENAENA ENVQSGNVA	NSQPALRNL	SKNTNAVLSN
Consensus	-----L-	S---N---S-	
	1701		1750
Hap	LSA.....TV NSMLSVQDEL	DRL.FVDQAO	SAVWTNIAQD KRRYDSDAFR
HK368IGA	ARAKAQFVAL NVGKAVSQHI	SQLEMNEGQ	YNVWVSNTSM NKNYSSSQYR
HK393IGA	ARAKAQFVAL NVGKAVSQHI	SQLEMNEGQ	YNVWVSNTSM NKNYSSSQYR
HK715IGA	AMAKAQFVAL NVGKAVSQHI	SQLEMNEGQ	YNVWVSNTSM NENYSSSQYR
HK61IGA	AMAKAQFVAL NVGKAVSQHI	SQLEMNEGQ	YNVWISNTSM NKNYSSSEQYR
Consensus	--A-----N---V---L-----Q--VW-----Y-S---R		

FIGURE 7G

	1751		1800
Hap	AYQQQKTNLR QIGVQKALAN GRIGAVFSHS RSDNTFDEQV KNHATLTIMS		
HK368IGA	RESSKSTQTQ LGWDQTISNN VOLGGVFTYV RNSNNFDKAT SKN.TLAQVN		
HK393IGA	RESSKSTQTQ LGWDQTISNN VOLGGVFTYV RNSNNFDKAT SKN.TLAQVN		
HK715IGA	RESSKSTQTQ LGWDQTISNN VOLGGVFTYV RNSNNFDKAS SKN.TLAQVN		
HK61IGA	RESSKSTQTQ LGWDQTISNN VOLGGVFTYV RNSNNFDKAS SKN.TLAQVN		
Consensus	-----T-----Q-----N---G-VF---R--N-FD--- ----TL----		
	1801		1850
Hap	GFAQYQWGD L QF..GVNVGT GISASKMAEE QSRKIHRKAI NYGVNASYQF		
HK368IGA	FYSKY.YADN HWYLGIDLGY GKFQSKLQTN HNAKFARHTA QFGLTAGKAF		
HK393IGA	FYSKY.YADN HWYLGIDLGY GKFQSKLQTN HNAKFARHTA QFGLTAGKAF		
HK715IGA	FYSKY.YADN HWYLGIDLGY GKFQSNLQTN HNAKFARHTA QFGLTAGKAF		
HK61IGA	FYSKY.YADN HWYLGIDLGY GKFQSNLQTN HNAKFARHTA QFGLTAGKAF		
Consensus	----Y--D- ----G--G- G--S----- --K--R-- --G--A--F		
	1851		1900
Hap	RLGQLGIOPY FGVNRYFIER ENYQSEEV RV KTPSLAFNRY NAGIRVDYTF		
HK368IGA	NLGNEFGITPI VGVRYSYLSN ADFALDQARI KVNPISVKTA FAQVDLSYTY		
HK393IGA	NLGNEFGITPI VGVRYSYLSN ADFALDQARI KVNPISVKTA FAQVDLSYTY		
HK715IGA	NLGNEFGITPI VGVRYSYLSN ANFALAKDRI KVNPISVKTA FAQVDLSYTY		
HK61IGA	NLGNEFAVKPT VGVRYSYLSN ADFALADRI KVNPISVKTA FAQVDLSYTY		
Consensus	-LG-----P- -GV-----R- K----- -A-----YT-		
	1901		1950
Hap	TPTDNISVKP YFFVNYVDVS NANVQITVNL TVLQQPFGRY WQKEVGLKAE		
HK368IGA	.HLGEFSVTP ILSARY.DAN QGSGKINVNG YDFAYNVENQ QQYNAGLKLK		
HK393IGA	.HLGEFSVTP ILSARY.DAN QGSGKINVNG YDFAYNVENQ QQYNAGLKLK		
HK715IGA	.HLGEFSVTP ILSARY.DTN QGSGKINVNQ YDFAYNVENQ QQYNAGLKLK		
HK61IGA	.HLGEFSITP ILSARY.DAN QGNGKINVS V YDFAYNVENQ QQYNAGLKLK		
Consensus	-----S--P -----Y-D- -----V-- ----- -Q--GLK--		
	1951		1982
Hap	ILHFQISAFI SKSQGSQLGK QQNVGVKLG Y RW		
HK368IGA	YHNVKLSLIG GLTKAKQAEK OKTAELKLSF SF		
HK393IGA	YHNVKLSLIG GLTKAKQAEK OKTAELKLSF SF		
HK715IGA	YHNVKLSLIG GLTKAKQAEK OKTAELKLSF SF		
HK61IGA	YHNVKLSLIG GLTKAKQAEK OKTAEVKLSF SF		
Consensus	-----S--- -----Q-K Q-----KL-- --		

FIGURE 7H



Fig. 8

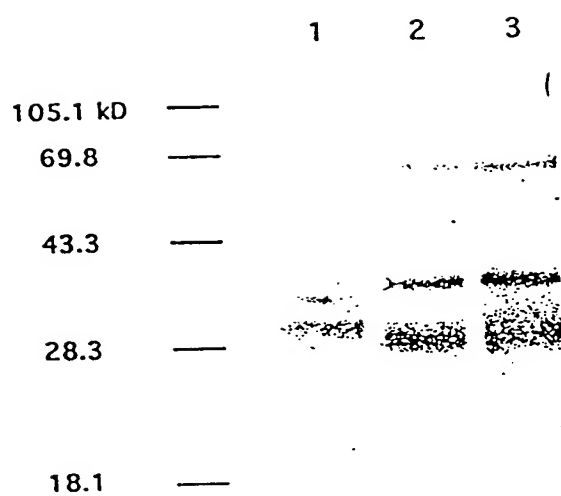


FIGURE 8

Fig. 9

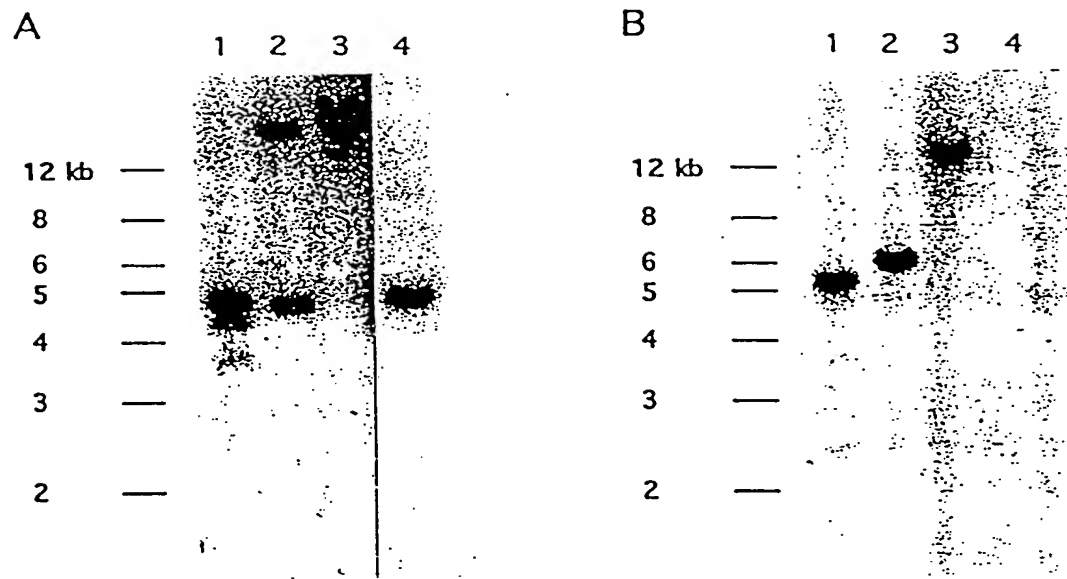
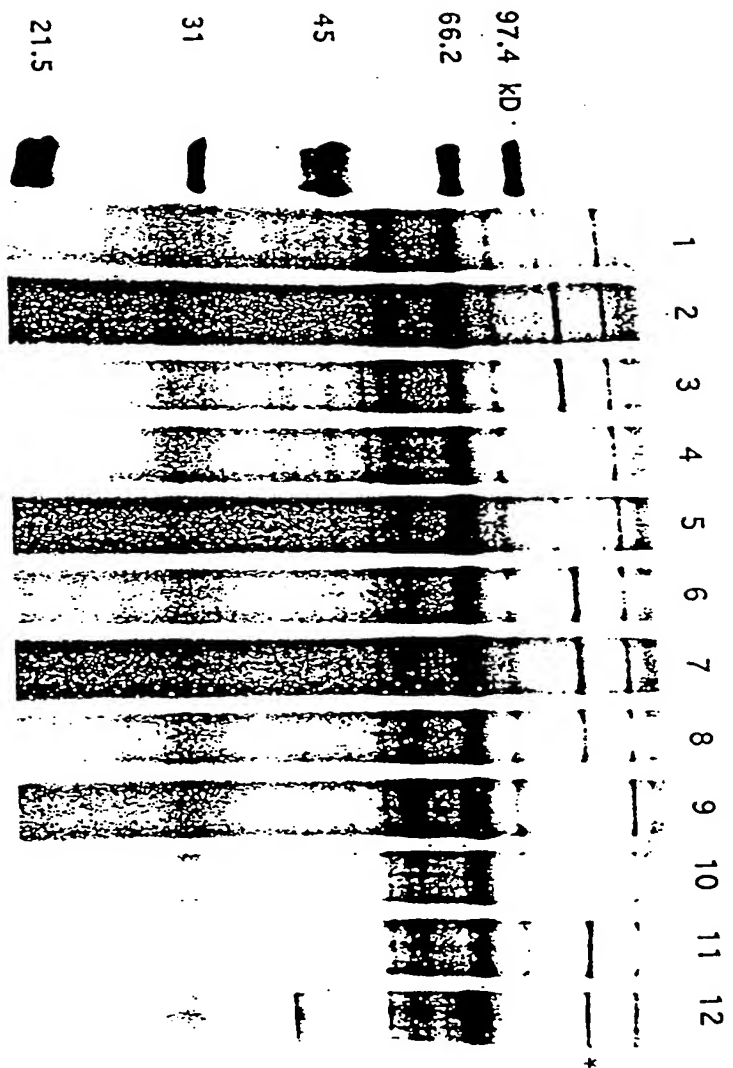


FIGURE 9

Fig. 10



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FIGURE 10  
—

		1	50
HapN187	(1)	MKKTVFRNLNFLTACISLGIVSQAWAGHTYFGIDYQYYRDFAEKNGKFTVVG	
HapTN106	(1)	MKKTVFRNLNFLTACISLGIVSQAWAGHTYFGIDYQYYRDFAEKNGKFTVVG	
Hap860295	(1)	MKKTVFRNLNFLTACISLGIVSQAWAGHTYFGIDYQYYRDFAEKNGKFTVVG	
Consensus	(1)	MKKTVFRNLNFLTACISLGIVSQAWAGHTYFGIDYQYYRDFAEKNGKFTVVG	
		51	100
HapN187	(51)	AQNLKVYNNKQGLVCTSMTRKAPMIDFSVVSRRNGVAALV ENQYTVSVAHNV	
HapTN106	(51)	ACDLDIYNNKQGLVCTSMTRKAPMIDFSVVSRRNGVAALV ENQYTVSVAHNV	
Hap860295	(51)	AKNTEVYNNKQGLVCTSMTRKAPMIDFSVVSRRNGVAALV GDQYTVSVAHNV	
Consensus	(51)	A I YNNK G GT M PM D S R G L Q SVAHN	
		101	150
HapN187	(101)	GYTDVDFGAEENPDQHRFTYKIVKRNNYK KDNLHPEYEDDYHNPRLHKFTV	
HapTN106	(101)	GYDVDVDFGMEGENPDQHRFKIVKRNNYKSC--DROYNQYQHRLEKFTV	
Hap860295	(101)	GYNSVDFGAEENPDQHRFTYQIVKRNNYK PKDNPEYHGDYHMPRLHKFTV	
Consensus	(101)	GY VDFG EG NPDQHRF Y VKR NYK DY PRL KFTV	
		151	200
HapN187	(151)	PEAAPTIDMTSNMNGSTYSERTKYPERVRVCSGRCTFRNDQK---GDQ---	
HapTN106	(149)	PEAAPTIDMTSNMNGSTYSERTKYPERVRVCSGRCTFRNDQK---GDQ---	
Hap860295	(151)	IDAETIAKMTIDNMNGKNYADLSKYEDRVRVCSGRCTFRNDQK---GDQ---	
Consensus	(151)	T P M M G Y YP RVR G G Q W D G	
		201	250
HapN187	(196)	VAGAYHYLTAGNTHNRCAGNGYSYLGEDVRKAGEYGPPLIAGSKGDSGS	
HapTN106	(195)	LA YGGSWLIGGNTFEDGPAGNGHLELNRVONPNKYGPPLIAGSGGDSGS	
Hap860295	(201)	LA DAYLWRIAGNTHSOSGAGNGHVNLSGDIKPNNYGPPLIAGSGGDSGS	
Consensus	(201)	A GNT AGNG L G YGPLP S GDSGS	
		251	300
HapN187	(246)	PMFIYDAEKOKWLLNG ILREGNPEEGKENGFOIRKNSYFDE-LEERDLHT	
HapTN106	(245)	PMFIYDKEVKKWLNGVLRGNPYAAVGN SYCITRKDMFOG-LLNQDITA	
Hap860295	(251)	PMFIYDAIKOKWLLNGVLTQENPEFGAGNGFOIRKNWEYDNVEVEDLPI	
Consensus	(251)	PMFIYD KWL NG L GNP N Q RK F D	
		301	350
HapN187	(295)	SLYTRAGNGVYTTSGNDNG-----QCSIQKSGIPSETKITLANMSIPLK	
HapTN106	(294)	NEWDTNAEYRFNIGSDHNGRVATIKSTLPKKAIQPERIVGLYDNSOIHDA	
Hap860295	(301)	TELEPRSNCHYSFTSNNG-----TCTVLTQNEKVSMPQFKVRTVOLFNE	
Consensus	(301)	NG L	
		351	400
HapN187	(340)	-EKDKVHNERYDGL--NLSRPRINNGETLYEMDQKQESLIIFASDINQAG	
HapTN106	(344)	RDKNGDESPSYKGP--NPWSEALHHGKSIYFGDOCTCTPTIENNINQAG	
Hap860295	(346)	ALKEKDKEPVYAAGGVNAYKPRINNGKNLYEGDRCTGTLPIENNINQAG	
Consensus	(351)	K P Y N P L G YF D G L INQAG	
		401	450
HapN187	(387)	GLYFEGNETVS PNSSN-OTWOGAGIHVSENSTVTWKVNGVEHDRLSKIGKG	
HapTN106	(392)	GLYFEGNEVVKGNQNNITWOGAGVSVGEESTVEWQVHNPEGDRLSKIGLG	
Hap860295	(396)	GLYFEGNETVS SENN-ATWOGAGVHVGE DSTVTWKVNGVEHDRLSKIGKG	
Consensus	(401)	GLYFEGNF V N TWOGAG V E STV W V E DRLSKIG G	

FIG. 11A

		451		500
HapN187	(436)	ILHVOAKGKIN KESISVGDCKVTL EQQAD DQGNKOAF SEI ELVSGR GIVOL		
HapTN106	(442)	TL LVNGKCKNLES LSVGNGLV VL DQQADE SCOKOAFKKEVGI VSGRATVQL		
Hap860295	(445)	TL EIQAKGKINLGSISVGDCKVTL DQQADE NNOKOAFKKEVGI VSGRATVQL		
Consensus	(451)	TL KG N GS SVG G V L QQAD KQAF E G VSGR TVQL		
		501		550
HapN187	(486)	NDDK EFTDKF YFGFRGGR L DLNGHSLTFKRTONT DEGAMIVNHNTTO AA		
HapTN106	(492)	NSADQVDPNNT YFGFRGGR L DLNGHSLTF E LONTDEGAMIVNHN ASOTA		
Hap860295	(495)	NSADQVDPNNT YFGFRGGR L DLNGHSLTFKRTONT DEGAMIVNHNTTO VA		
Consensus	(501)	N Q D YFGFRGGR L DLNGHSLTF RIQNTDEGAMIVNHN Q A		
		551		600
HapN187	(536)	NVTTGNESV VLE NGNNINKLDY RKEIAYNCWFGETDKNKHNGRLNLIY		
HapTN106	(542)	NTTTGN ATINS-----DSKQITNKLDIA ENWFGE QDKATNGRLN VNY		
Hap860295	(545)	NTTTGNESV TAPSNKNNINKLDY SKETAYNCWFGETE ENKHNGRLNLIY		
Consensus	(551)	N TITGN I L K IA NGWFE D K NGRLN Y		
		601		650
HapN187	(585)	KPTTEDRTLLLSGGTNLKG DPTQTKKLEFSGRPTPHAYNHL KRWSEME		
HapTN106	(587)	QPVNAENHLLLSGGTNL NENITQNGCTLVFSGRPTPHAYNHL REDLSNME		
Hap860295	(595)	KPTTEDRTLLLSGGTNLKGNTQ EGGTLVFSGRPTPHAYNHLNR --PNEL		
Consensus	(601)	P LLLSGGTNL G ITQ G L FSGRPTPHAYNHL		
		651		700
HapN187	(635)	GI PQGEI VWDHDWINKT FKAENFQIKGGS AVVSRNVSSIEGNWTVSNNAN		
HapTN106	(637)	GI PQGEI VWDHDWINKT FKAENFQIKGGS AVVSRNVSSIEGNWTVSNNAN		
Hap860295	(643)	GR PQGE VVIEDDWITRT FKAENFQIKGGS AVVSRNVSSIEGNWTVSNNAN		
Consensus	(651)	G PQGE V D DWI RTFKAENFQIKGGS AVVSRNVSSIEGNWTVSNNAN		
		701		750
HapN187	(685)	AATFGVVPNQONTICTRSDWTGLTTC OKVDLTDKVINSIP KIQNGSINL		
HapTN106	(687)	AATFGVVPNQONTICTRSDWTGLTTC KVDLTDKVINSIP KIQNGSINL		
Hap860295	(693)	AATFGVVPNQONTICTRSDWTGLTTC KVDLTDKVINSIP KIQNGSINL		
Consensus	(701)	A FGVVPNQONTICTRSDWTGLTTC VDLTD KVINSIP IQNGSINL		
		751		800
HapN187	(735)	TDNAT ANVKGLAKLNGNVTL THSQFTLSNNATQ IENIRLS DNSTATVDN		
HapTN106	(737)	TDNATVNTLHGLAKLNGNVTL DHSQFTLSNNATOTGNI KLSNHNATVDN		
Hap860295	(743)	TDNATVNTLHGLAKLNGNVTL THSQFTLSNNATOTGNI OLSNHNATVDN		
Consensus	(751)	TDNAT N GLAKLNGNVTL HSQFTLSNNATQ GNI LS ATVDN		
		801		850
HapN187	(785)	ANLNGNVHLTDSAQFSLKNSHFSHQIQGK GTTVPLENATWTMPSDTLQ		
HapTN106	(787)	ANLNGNV NLMPSAQFSLKNSHFSHQIQG GEDTTVMLENATWTMPSDTLQ		
Hap860295	(793)	ANLNGNVHLTDSAQFSLKNSHFSHQIQGKDTTVPLENATWTMPSD ARLQ		
Consensus	(801)	ANLNGNV L DSAQFSLKNSHFSHQIQG TTV LENATWTMPSD TLQ		
		851		900
HapN187	(835)	NLTENNST I TENSAYSASSNNTPRRRRRSLETETPTSAEHRFNTLTVNG		
HapTN106	(837)	NLTENNSTVTLNSAYSAS ISNNAPRRRRRSLETETPTSAEHRFNTLTVNG		
Hap860295	(843)	NLTENNSTVTLNSAYSASSNNAPR -HRRSLETETPTSAEHRFNTLTVNG		
Consensus	(851)	NLTENNST TLNSAYSAS SNN PR RRSLETETPTSAEHRFNTLTVNG		

FIG. 11B

		901		950
HapN187	(885)	KLSGQCTFOFTSSSLFGYKSDKLLSNDAGDY ILSVRNTGKEPETLEOLT		
HapTN106	(887)	KLSGQCTFOFTSSSLFGYKSDKLLSNDAGDYILSVRNTGKEP VIIFGOLT		
Hap860295	(892)	KLSGQCTFOFTSSSLFGYKSDKLLSNDAGDYILSVRNTGKEPE ALEOLT		
Consensus	(901)	KLSGQGTFOFTSSSLFGYKSDKLLSNDAGDY LSVRNTGKEP QLT		
		951		1000
HapN187	(935)	LVESKDN QPLSDKLEKFTLENDHVDAGALRYKLVKNDCGEFRLHNPIKEOEL		
HapTN106	(937)	LVESKDNKPLSDKL TETLENDHVDAGALRYKLVKNDCGEFRLHNPIKEOEL		
Hap860295	(942)	LVESKDNKPLSDKLEKFTLENDHVDAGALRYKLVKN NSEFRLHNPIKEOEL		
Consensus	(951)	LVESKDN PLSDKL FTLENDHVDAGALRYKLVKN GEFRLHNPIKEOEL		
		1001		1050
HapN187	(985)	HNDLVRAEQAERTLEAKQVE PIAKTQI GEPKVRSRRAARAAPDITLPDOS		
HapTN106	(987)	RSDLVRAEQAERTLEAKQVEQTAKTQTS KARVRSP --- RAVESDPLPAOS		
Hap860295	(992)	RNDLVRAEQAERTLEAKQVEQTA ETQTSNARVRSK --- RAVESDITLPDOS		
Consensus	(1001)	DLVRAEQAERTLEAKQVE TA TQT VRS RA F D LP QS		
		1051		1100
HapN187	(1035)	LLN ALEAKOAELETAETQKS KAKTKKVRSKRAV --- FSDPLLDOS		
HapTN106	(1034)	LLKALEAKOA - LITETQTS --- KAKKVRSKRAAREFSDTLPDO		
Hap860295	(1039)	QLDVLQAEQVEPIAEKOKN --- KAKKVRSKRAV --- FSDITLPDOS		
Consensus	(1051)	L L A Q T E Q K K KVRSKRA FSD L DQ		
		1101		1150
HapN187	(1076)	----- IFALEAALEVIDA PQ		
HapTN106	(1073)	----- I LOAALEVIDAQO		
Hap860295	(1085)	EQVEPTAEKQKNKAKKVRSKRAAREFSDTPLDLR IKVLEVKLEVINAOO		
Consensus	(1101)	L LEVI A Q		
		1151		1200
HapN187	(1091)	QSEKDRLAQEEAEK - ORKOKDLISRYSNSALSSELSATVNSMLSVQDELDR		
HapTN106	(1086)	QVKKEPOTQEEEEKRORKOKELISRYSNSALSSELSATVNSMLSVQDELDR		
Hap860295	(1135)	QVKKEPQDQ --- EK - ORKOKDLISRYSNSALSSELSATVNSMLSVQDELDR		
Consensus	(1151)	Q K Q EK QRKQK LISRYSNSALSSELSATVNSMLSVQDELDR		
		1201		1250
HapN187	(1140)	LFVDQAQSAVWTNIAQDKRRYDSDAFRAYQOKTNLROIGVQKALANGRIG		
HapTN106	(1136)	LFVDQAQSAVWTNIAQDKRRYDSDAFRAYQOKTNLROIGVQKAL DNGRIG		
Hap860295	(1181)	LFVDQAQSAVWTNIAQDKRRYDSDAFRAYQOKTNLROIGVQKALANGRIG		
Consensus	(1201)	LFVDQAQSAVWTNIAQDKRRYDSDAFRAYQOKTNLRQIGVQKAL NGRIG		
		1251		1300
HapN187	(1190)	AVFHSRSRSDNTFDEQVKNHATLTMMSCFAQYQWGDLOFGVNVGTGISASK		
HapTN106	(1186)	AVFHSRSRSDNTFDEQVKNHATL AMMSGFAQYQWGDLOFGVNVG AGISASK		
Hap860295	(1231)	AVFHSRSRSDNTFDEQVKNHATLTMMSCFAQYQWGDLOFGVNVGTGISASK		
Consensus	(1251)	AVFHSRSRSDNTFDEQVKNHATL MMSGFAQYQWGDLOFGVNVG GISASK		
		1301		1350
HapN187	(1240)	MAEEQSRKTHRKAINYGVNASYOERLGOLGIOPYEGVNRIFYERENYQSE		
HapTN106	(1236)	MAEEQSRKTHRKAINYGVNASYOERLGOLGIOPY LGVNRIFYERENYQSE		
Hap860295	(1281)	MAEEQSRKTHRKAINYGVNASYOERLGOLGIOPYEGVNRIFYERENYQSE		
Consensus	(1301)	MAEEQSRKIHRKAINYGVNASYOERLGOLGIOPY GVNRYFIERENYQSE		

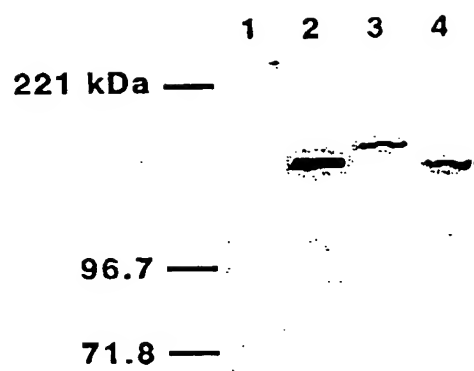
FIG. 11C

		1351		1400
HapN187	(1290)	EV R V K T I P S L A E N R Y N A G I R V D Y T F T P T D N I S V K P Y F F V N Y V D V S N A N V Q T		
HapTN106	(1286)	EV K V Q T P S L V E N R Y N A G I R V D Y T F T P T D N I S I K P Y F F V N Y V D V S N A N V Q T		
Hap860295	(1331)	EV K V K T I P S L A E N R Y N A G I R V D Y T F T P T D N I S V K P Y F F V N Y V D V S N A N V Q T		
Consensus	(1351)	EV V T P S L F N R Y N A G I R V D Y T F T P T D N I S K P Y F F V N Y V D V S N A N V Q T		
		1401		1450
HapN187	(1340)	T V N L F V L Q Q P F G R Y W Q K E V G L K A E I L H F Q I S A F I S K S Q G S Q L G K Q Q N V G V		
HapTN106	(1336)	T V N R T M L Q Q S E G R Y W Q K E V G L K A E I L H F Q L S A F I S K S Q G S Q L G K Q Q N V G V		
Hap860295	(1381)	T V N S F V L Q Q P F G R Y W Q K E V G L K A E I L H F Q L S A F I S K S Q G S Q L G K Q Q N V G V		
Consensus	(1401)	T V N T L Q Q F G R Y W Q K E V G L K A E I L H F Q S A F I S K S Q G S Q L G K Q Q N V G V		
		1451		
HapN187	(1390)	K L G Y R W		
HapTN106	(1386)	K L G Y R W		
Hap860295	(1431)	K L G Y R W		
Consensus	(1451)	K L G Y R W		

FIG. 11D

Fig. 12

**A**



**B**





Fig. B

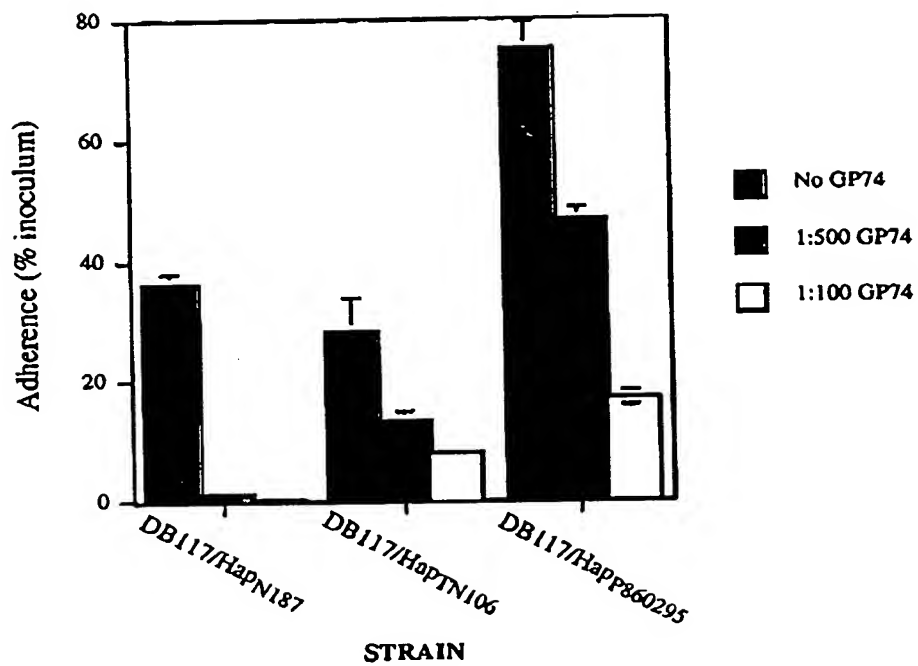


Fig 14

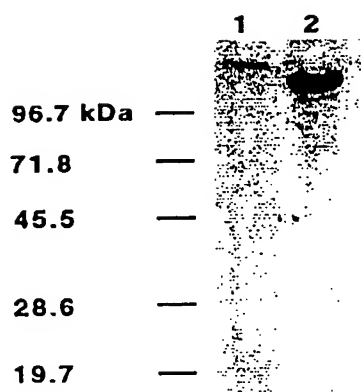
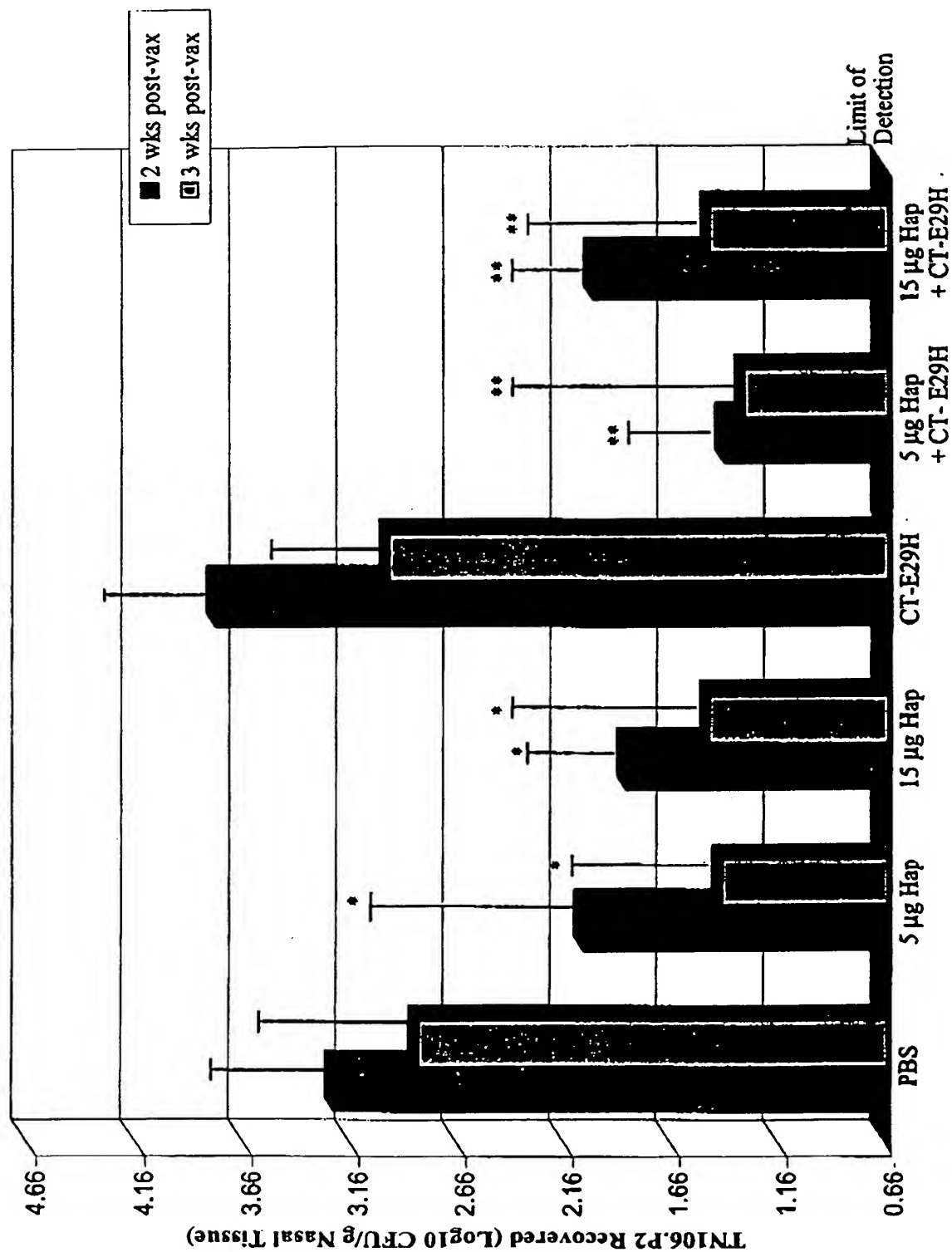


Fig 15



Nucleotide sequence for NTHi strain 11 hap gene (start codon to stop codon):

```

1  ATGAAAAAAA CTGTATTTTCG TCTTAATTTT TTAACCGCTT GCATTTTCATT
51  AGGGATAGTA TCGCAAGCGT GGGCAGGTCA TACTTATTTT GGGATTGACT
101  ACCAATATTA TCGTGATTTT GCCGAGAATG AAGGCAAGTT TGCAGTTGGG
151  GCTAAAAATA TTGATGTTTA TAACAAAGAA GGGCAATTAG TTGGCACATC
201  AATGACAAAA GCCCCGATGA TTGATTTCTC AGTCGTTTCC AGAAATGGAG
251  TTGCTGCCTT AGTAGGCGAT CAGTATATTG TGAGTGTGGC ACATAATGTA
301  GGCTATACCA ATGTGGATT TGGTGCTGAA GGACAAAATC CTGATCAACA
351  TCGTTTTACT TATAAAATTG TGAAACGGAA TAATTATAAT CACGATGCGA
401  AGCACCCTA TCTAGATGAC TACCATAATC CACGTTTACA TAAATTTGTA
451  ACGGATGCGG CACCAATTGA TATGACTTCA CATATGGATG GCAATAAGTA
501  TGCAAATAAG GAAAAATATC CTGAACGAGT ACGCGTCGGA TCTGGAGATC
551  AGTATTGGGA TGACGATCAA AACAAACAGAA CTTATTTATC TGACGGATAT
601  AATTATTTAA CAGGTGGGAA TACATATAAT CAAAGCGGTA GAGGTGATGG
651  ATATTCATAT GTGAGAGGTG ATATTCGCAA AGTTGGCGAT TATGGTCCAT
701  TACCGATTGC AAGTTCATTC GGGGACAGTG GATCTCCAAT GTTTATTTAT
751  GATGCTGAAA CACAAAAATG gcTAATTAAT GGAGTATTGC GGGAGGGGCA
801  ACCTTATACA GGCGAATTCG ATGGATTTCA ATTAGCCCCG AAATCTTTCC
851  TTGATGAAAT TATACGCAA GATCAACCAA ATGGTTTTTT AACCCCTAAG
901  GGGAATGGCG TTTATACCAT TTCTAAAGT GACGATGGGA TAGGAGTTGT
951  TACTTCGAAA ATTGGAAAAC CTCGTGAAAT ACCTTTAGCG AACACAAAT
1001  TAAAAATAGA AGATAAAGAT ACTGTCTATA ATAACAGATA TAATGGTCCT
1051  AATATTTATT CTCCTCAATT AAACAATGGC AAGAATATTT ATTTTGGAGA
1101  TGAAGAATTA GGATCCATAA CTTTAACGAC TGATATCGAT CAAGGTGCAG
1151  GCGGTTTGTA TTTTGAGGGG GATTTTATAG TTTCGCCTAC CAAAAATGAA
1201  ACGTGGAAG GTGCGGGCAT TCATGTCAGT GAAATTAGTA CCGTTACTTG
1251  GAAAGTAAAC GGCGTGGAAA ATGATCGACT TTCTAAAATC GGTAAAGGAA
1301  CATTACACGT TAAAGCCAAA GGGGAAAATA AAGGTTTCGAT CAGCGTAGGC
1351  GATGGTAAAG TCATTTTGGA GCAGCAGGCA GACGATCAAG GCAACAAACA
1401  AGCCTTTAGT GAAATTGGCT TGGTTAGCGG CAGAGGGACT GTTCAATTAA
1451  ACGATGATAA ACAATTTGAT ACCGATAAAT TTTATTTTCG CTTTCGTGGT
1501  GGTCGCTTAG ATCTTAACGG ACATTCATTA ACCTTTAAAC GTATCCAAAA
1551  TACGGACGAG GGGGCGATGA TTGTGAACCA TAATACAACT CAAGTCGCTA
1601  ATATTACTAT TACTGGGAAC GAAAGTATTA CTGCTCCATC TAATAAAAAT
1651  AATATTAATA AACTTGATTA CAGCAAAGAA ATTGCCTACA ACGGCTGGTT
1701  TNGCGAAACA GATAAAAATA AACATAATGG ACGATTAAAC CTTATTTATA
1751  AACCAACCAC AGAAGATCGT ACTTTGCTAC TTTCAGGCGG CACAACTTA
1801  AAAGGCGATA TTAATAAAC AAAAGGTAAA CTATTTTTCG GCGGTAGACC
1851  GACACCCAC GCCTACAATC ATTTAGACAA ACGTTGGTCA GAAATGGAAG
1901  GTATCCCACA AGGCGAAATT GTGTGGGATT ACGATTGGAT TAACCGCACA
1951  TTTAAAGCTG AAAACTTCCA AATTAAAGGC GGAAGTTCGG TGGTTTCTCG
2001  CAATGTTTCT TCAATTGAGG GAAATTGGAC AGTCAGCAAT AATGCAAATG

```

Fig. 16A

2051 CCACATTTGG TGTGTGCCA AATCAGCAAA ATACCATTG CACGCGTTCA  
 2101 GATTGGACAG GATTAACGAC TTGTAAAACA GTTAATTTAA CCGATAAAAA  
 2151 AGTTATTGAT TCCATACCGA CAACACAAAT TAATGGTTCT ATTAATTTAA  
 2201 CTGATAATGC AACAGTGAAT ATTAATGGTT TAGCAAAACT TAATGGTAAT  
 2251 GTCACTTTAA TAAATCATAG CCAATTTACA TTGAGCAACA ATGCCACCCA  
 2301 AATAGGCAAT ATCAAACCTT CAAATCACGC AAATGCAAGG GTAAATAATG  
 2351 CCACTTTAAT GGGCGATGTG AATTTAGCGG ATACTAGCCG TTTTACATTA  
 2401 AGCAATCAAG CAACACAGAT TGGCACAATC AGTCTTCATC AGCAAGCTCA  
 2451 AGCAACAGTG GATAATGCAA ACTTGAACGG TAATGTGCAT TTAACGGATT  
 2501 CTGCCAGATT TTCTTTAAAA AACAGTCATT TTTCGCACCA AATTCAGGGC  
 2551 GACAAAGACA CAACAGTGAC GTTGGAAAAT GCGACTTGGA CAATGCCTAG  
 2601 CGATACTACA TTGCAGAATT TAACGCTAAA TAATAGTACT GTTACGTAA  
 2651 ATTCAGCTTA TTCAGCTAGC TCAAATAATG CGCCACGTCG CCgCCGTTCA  
 2701 TTAGAGACGG AAACAACGCC AACATCGGCA GAACATCGTT TCAACACATT  
 2751 GACAGTAAAT GGTAAATTGA GCGGGCAAGG CACATTCCAA TTTACTCCAT  
 2801 CTTTATTTGG CTATGAAAGC GATAAATTAA AATTATCCAA TGACGCTGAG  
 2851 GCGGATTACA CATTATCTGT TCGCAACACA GGCAAAGAAC CCGTGACCCT  
 2901 TGAGCAATTA ACTTTGGTTG AAAGCAAAGA TAATAAACCG TTATCAGACA  
 2951 AACTCAAAT TACTTTAGAA AATGACCACG TTGATGCAGG TGCATTACGT  
 3001 TATAAATTAG TGAAGAATAA GGGCGAATTC CGCTTGATA ACCCAATAAA  
 3051 AGAGCAGGAA TTGCGCTCTG ATTTAGTAAG AGCAGAGCAA GCAGAACGAA  
 3101 CATTAGAAGC CAAACAAGTT GAACAGACTG CTGAAACACA AACAGTAAT  
 3151 GCAAGAGTGC GGTCAAGAAG AGCGGTGTTG TCTGATACCC CGTCTGCTCA  
 3201 AAGCCTGTTA AACGCATTAG AAGTCAAACA AGCTGAACCG AATGCTAAAA  
 3251 CACAAAAAAG TAAGGCAAAA ACAAAAAAAG CGCGGTCAAA AAGAGCATTG  
 3301 AGAGAAGCGT TTTCTGATAC CCCGCCTGAT CTAAGCCAGT TAAACGTATT  
 3351 AGAAGCCGCA CTTAAGGTTA TTAATGCCCC ACCGCAAACA GAAAAAGAAC  
 3401 GTCAAGCTCA AGAGGAAGAA GCGAAAAGAC AACGCaACA AAAAGACTTG  
 3451 ATCAGCCGTT ACTCAAATAG TGC GTTATCG GAGTTGTCTG CAACAGTAAA  
 3501 TAGTATGCTT TCCGTTCAAG ATGAATTGGA TCGTCTTTTT GTAGATCAAG  
 3551 CACAATCTGC CCTGTGGACA AATATCGCAC AGGATAAAAG ACGCTATGAT  
 3601 TCTGATGCGT TCCGTGCTTA TCAGCAGAAA ACGAACTTGC GTCAAATTGG  
 3651 GGTGCAAAAA GCCTTAGATA ATGGACGAAT TGGGGCGGTT TTCTCGCATA  
 3701 GCCGTTTACA TAATACCTTT GACGAACAGG TTAAAAATCA CGCGACATTA  
 3751 ACGATGATGT CGGGTTTTGC CCAATATCAA TGGGGCGATT TACAATTTGG  
 3801 TGTAACAGTG GGCGCGGGAA TTAGTGCGAG TAAAATGGCT GAAGAACAAA  
 3851 GCCGAAAAAT TCATCGAAAA GCGATAAATT ATGGTGTGAA TGCAAGTTAT  
 3901 CAGTTCCGTT TAGGGCAATT GGGTATTCAG CCTTATTTGG GTGTTAATCG  
 3951 ATATTTTATT GAACGTGAAA ATTATCAATC TGAAGAAGTG AAAGTGCAAA  
 4001 CACCGAGCCT TGCATTTAAT CGCTATAATG CTGGCATTCG AGTTGATTAT  
 4051 ACATTTACCC CGACAGATAA TATCAGCGTT AAGCCTTATT TCTTTGTCAA  
 4101 TTATGTTGAT GTTTCAAACG CTAACGTACA AACCCTGTA AATAGCACGA  
 4151 TGTTGCAACA ATCATTTGGG CGTTATTGGC AAAAAGAAGT GGGATTAAAG  
 4201 GCAGAAATTT TACATTTCCA ACTTTCCGCT TTTATCTCAA AATCTCAAGG

Fig. 16B

4251 TTCACAACTC GGTAACAGC AAAATGTGGG CGTGAAATTG GGCTATCGTT  
4301 GGTA

Fig. 16C

Amino acid sequence for NTHi strain 11 Hap protein (first amino acid to last amino acid):

```

 1  MKKTVFRLNF LTACISLGIV SQAWAGHTYF GIDYQYYRDF AENEGKFAVG
51  AKNIDVYNKE GQLVGTSMTK APMIDFSVVS RNGVAALVGD QYIVSVAHNV
101 GYTNVDFGAE GQNPdqhrft YKIVKRNNYN HDAKHRYLDD YHNPRLHKFV
151 TDAAPIDMTS HMDGNKYANK EKYPERVVRG SGDQYWDDDQ NNRTYLSDBGY
201 NYLTGGNTYN QSGRGDGYSY VRGDIRKVGd YGPLPIASSF GDSGSPMFIY
251 DAETQKWLIN GVLREGQPYT GEFDGFQLAR KSFLDEIIRK DQPNGFLTPK
301 GNGVYTISKS DDGIGVVTsk IGKPREIPLA NNKLKIEDKD TVYNNRYNGP
351 NIYSPQLNNG KNIYFGDEEL GSITLTDDID QGAGGLYFEG DFIVSPTKNE
401 TWKGAGIHVS EISTVTWKVN GVENDRLSKI GKGTlHVkAK GENKGSISVG
451 DGKVILEQQA DDQGNKQAFS EIGLVSGRGT VQLNDDKQFD TDKFYFGFRG
501 GRDLNGLHSL TFKRIQNTDE GAMIVNHNTT QVANITITGN ESITAPSNKN
551 NINKLDYSKE IAYNGWFXET DKNKHNGRLN LIYKPTTEDR TLLLSGGTNL
601 KGDITQTKGK LFFSGRPTPH AYNHLDKRWS EMEGIPQGEI VWDYDWINRT
651 FKAENFQIKG GSAVVSrNVs SIEGNWTVSN NANATFGVVP NQQNTICTRS
701 DWTGLTTCKT VNLTDKKVID SIPTTQINGS INLTdNATVN INGLAKLNGN
751 VTLINHSQFT LSNnATQIGN IKLSNHANAR VNNATLMGDV NLADTSRFTL
801 SNQATQIGTI SLHQQAQATV DNANLNGNVH LTDSARFSLK NSHFSHQIQG
851 DKDTTVTLEN ATWTMPsDTT LQNLTLNNST VTLNSAYSAS SNNAPRRRRS
901 LETETTPTSA EHRFNTLTVN GKLSGQGTfQ FTPSLFGYES DKLKLSNDAE
951 GDYTLsVRNT GKEPVTLEQL TLVESKDNKP LSDKLKFTLE NDHVDAGALR
1001 YKLvKNKGef RLHNPIKEQE LRSDLVRAEQ AERTLEAKQV EQTAETQTSN
1051 ARVRSRRAVL SDTPSAQSLl NAEVVKQAEp NAKTQKSKAK TKKARSKRAL
1101 REAFSDTPPD LSQlNVLEAA LKVINAQPQT EKERQAQEEE AKRQRKQKDL
1151 ISRYSNSALS ELSATVNSML SVQDELDRLF VDQAQsALWT NIAQDKRRYD
1201 SDAFRAYQOK TNLRQIGVQK ALDNGRIGAV FSHSRSDNTF DEQVKNHATL
1251 TMMSGFAQYQ WGDlQFGVNV GAGISASKMA EEQSRKIHRK AINyGVNASY
1301 QFRLGQLGIQ PYLGVNRYFI ERENYQSEEV KVQTPSLAFN RYNAGIRVDY
1351 TFTPtdNISV KPYFFVNYVD VSNANVQTTV NSTMLQQSFG RYWQKEVGLK
1401 AEILHFQLSA FISKsQGSQl GKQQNVGVKL GYRW

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Fig. 17

Nucleotide sequence for NTHi strain TN106 hap gene (start codon begins at position 422, stop codon begins at position 4595):

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1   TGGCGGCGGA CAAATTATTG CGACGGGTAC ACCAGAACAA GTTGCTAAAG
51  TAAAAAGTTC CCACACCGCT CGCTTCCTTA AACCGATTTT AGAAAAACCT
101 TAGAAAAAAT GACCGCACTT TCAGAGAAAA CTCACATAAA GTGCGGTTAT
151 TTTATTAGTG ATATTGTTTT AATTTTAGTT ATCTGTATAA ATTACATACA
201 ATATTAATCC ATCGCAAGAT TAGATTACCC ACTAAGTATT AAGCAAAAAC
251 CTAGAAATTT TGGCTTAATT ACTATATAGT TTTACTCATT TATTTTCTTT
301 TGTGCCTTTT AGTTCATTTT TTTAGCTGAA ATCCCTTAGA AAATCACCGC
351 ACTTTTATTG TTCAATAGTC GTTTAACCAC GTATTTTTTA ATACGAAAAA
401 TTACTTAATT AAATAAACAT TATGAAAAAA ACTGTATTTT GTCTGAATTT
451 TTTAACCGCT TGCATTTTCA TAGGGATAGT ATCGCAAGCG TGGGCAGGTC
501 ATACTTATTT TGGGATTGAC TACCAATATT ATCGTGATTT TGCCGAGAAT
551 AAAGGGAAGT TTACAGTTGG GGCTCAAGAT ATTGATATCT ACAATAAAAA
601 AGGGGAAATG ATAGGTACGA TGATGAAAGG TGTGCCTATG CCTGATTTAT
651 CTTCCATGGT TCGTGGTGGT TATTCAACAT TGATAAGTGA GCAGCATTTA
701 ATTAGCGTCG CACATAATGT AGGGTATGAT GTCGTTGATT TTGGTATGGA
751 GGGGGAAAAT CCAGACCAAC ATCGTTTTAA GTATAAAGTT GTTAAACGAT
801 ATAATTATAA GAGCGGTGAT AGACAATATA ATGATTATCA ACATCCAAGA
851 TTAGAGAAAT TTGTAACGGA AACTGCACCT ATTGAAATGG TTTCATATAT
901 GGATGGTAAT CATTACAAAA ATTTTAATCA ATATCCTTTG CGAGTTAGAG
951 TTGGAAGTGG GCATCAATGG TGGAAAGACG ATAATAATAA AACCATTGGA
1001 GACTTAGCCT ATGGAGGTTT ATGGTTAATA GGTGGAAATA CCTTTGAAGA
1051 TGGACCAGCT GGTAACGGTA CATTAGAATT AAATGGGCGA GTACAAAATC
1101 CTAATAAATA TGGTCCACTA CCTACGGCAG GTTCATTCGG GGATAGTGGT
1151 TCTCCAATGT TTATTTATGA TAAGGAAAGT AAGAAATGGT TATTAAATGG
1201 CGTGTTACGT GAAGGAAATC CTTATGCTGC AGTAGGAAAC AGCTATCAAA
1251 TTACACGAAA AGATTATTTT CAAGGTATTC TTAATCAAGA CATTACAGCT
1301 AATTTTGGG ATACTAATGC TGAATATAGA TTTAATATAG GGAGTGACCA
1351 CAATGGAAGA GTGGCAACAA TCAAAAGTAC ATTACCTAAA AAAGCTATTC
1401 AGCCTGAACG AATAGTGGGT CTTTATGATA ATAGCCAAC T CATGATGCT
1451 AGAGATAAAA ATGGCGATGA ATCTCCCTCT TATAAAGGTC CTAATCCATG
1501 GTCGCCAGCA TTACATCATG GGAAAAGTAT TTACTTTGGC GATCAAGGAA
1551 CAGGAAC TTT AACAAATTGAA AATAATATAA ATCAAGGTGC AGGTGGATTG
1601 TATTTTGAAG GTAATTTTGT TGTAAGAGGC AATCAAAATA ATATAACTTG
1651 GCAAGGTGCA GGCGTTTCTG TTGGAGAAGA AAGTACTGTT GAATGGCAGG
1701 TGCATAATCC AGAAGGCGAT CGCTTATCCA AAATTGGGCT GGGAACCTTA
1751 CTTGTTAATG GTAAAGGGAA AAACCTAGGA AGCCTGAGTG TCGGTAACGG
1801 TTTGGTTGTG TTAGATCAAC AAGCAGATGA ATCAGGTCAA AAACAAGCCT
1851 TTAAAGAAGT TGGCATTGTA AGTGGTAGAG CTACCGTTCA ACTAAATAGT
1901 GCAGATCAAG TTGATCCTAA CAATATTTAT TTCGGCTTTC GTGGTGGTCG
1951 CTTAGATCTT AATGGGCATT CATTAACTT TGAACGTATC CAAAATACGG
2001 ATGAAGGCGC GATGATTGTG AACCACAACG CTTCTCAAAC CGCAAATATT

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Fig. 18A



2051	ACGATTACAG	GCAACGCAAC	TATTAATTCA	GATAGCAAAC	AACTTACTAA
2101	TAAAAAAGAT	ATTGCATTTA	ACGGCTGGTT	TGGTGAGCAA	GATAAAGCTA
2151	AAACAAATGG	TCGTTTAAAT	GTGAATTATC	AACCAGTTAA	TGCAGAAAAT
2201	CATTTGTTGC	TTTCTGGGGG	GACAAATTTA	AACGGCAATA	TCACGCAAAA
2251	TGGTGGTACG	TTAGTTTTTA	GTGGTCGTCC	AACGCCTCAT	GCTTACAATC
2301	ATTTAAGAAG	AGACTTGTCT	AACATGGAAG	GTATCCCACA	AGGCGAAATT
2351	GTGTGGGATC	ACGATTGGAT	CAACCGCACA	TTTAAAGCTG	AAAACCTCCA
2401	AATTAAAGGC	GGAAGTGC GG	TGGTTTCTCG	CAATGTTTCT	TCAATTGAGG
2451	GAAATTGGAC	AGTCAGCAAT	AATGCAAATG	CCACATTGTTG	TGTTGTGCCA
2501	AATCAGCAAA	ATACCATTTG	CACGCGTTCA	GATTGGACAG	GATTAACGAC
2551	TTGTAAACA	GTTGATTTAA	CCGATAAAAA	AGTTATTAAT	TCCATACCGA
2601	CAACACAAAT	TAATGGTTCT	ATTAATTTAA	CTGATAATGC	AACAGTGAAT
2651	ATTCATGGTT	TAGCAAAACT	TAATGGTAAT	GTCACTTTAA	TAGATCACAG
2701	CCAATTTACA	TTGAGCAACA	ATGCCACCCA	AACAGGCAAT	ATCAAACTTT
2751	CAAATCACGC	AAATGCAACG	GTGGACAATG	CAAATTTGAA	CGGTAATGTG
2801	AATTTAATGG	ATTCTGCTCA	ATTTTCTTTA	AAAAACAGCC	ATTTTTCGCA
2851	CCAAATCCAA	GGTGGGGAAG	ACACAACAGT	GATGTTGGAA	AATGCGACTT
2901	GGACAATGCC	TAGCGATACC	ACATTGCAGA	ATTTAACGCT	AAATAATAGT
2951	ACTGTTACGT	TAAATTCAGC	TTATTTCAGT	ATCTCAAATA	ATGCGCCACG
3001	CCGTCGCCGC	CGTTCATTAG	AGACGGAAAC	AACGCCAACA	TCGGCAGAAC
3051	ATCGTTTCAA	CACATTGACA	GTAAATGGTA	AATTGAGCGG	GCAAGGCACA
3101	TTCCAATTTA	CTTCATCTTT	ATTTGGCTAT	AAAAGCGATA	AATTAAAAAT
3151	ATCCAATGAC	GCTGAGGGCG	ATTACACATT	ATCTGTTTCG	AACACAGGCA
3201	AAGAACCCGT	GACCTTTGGG	CAATTAACCT	TGGTTGAAAG	CAAAGATAAT
3251	AAACCGTTAT	CAGACAAACT	CACATTACAG	TTAGAAAATG	ACCACGTTGA
3301	TGCAGGTGCA	TTACGTTATA	AATTAGTGAA	GAATGATGGC	GAATTCCGCT
3351	TACATAACCC	AATAAAAGAG	CAGGAATTGC	GCTCTGATTT	AGTAAGAGCA
3401	GAGCAAGCAG	AACGAACATT	AGAAGCCAAA	CAAGTTGAAC	AGACTGCTAA
3451	AACACAAACA	AGTAAGGCAA	GAGTGCGGTC	AAGAAGAGCG	GTGTTTTCTG
3501	ATCCCCTGCC	TGCTCAAAGC	CTGTTAAAG	CATTAGAAGC	CAAACAAGCT
3551	CTGACTACTG	AAACACAAAC	AAGTAAGGCA	AAAAAAGTGC	GGTCAAAAAG
3601	AGCTGCGAGA	GAGTTTTCTG	ATACCCTGCC	TGATCAAATA	TTACAAGCCG
3651	CAC TTGAGGT	TATTGATGCC	CAACAGCAAG	TGAAAAAAGA	ACCTCAAACCT
3701	CAAGAGGAAG	AAGAGAAAAG	ACAACGCAAA	CAAAAAGAAT	TGATCAGCCG
3751	TTACTCAAAT	AGTGCGTTAT	CGGAGTTGTC	TGCGACAGTA	AATAGTATGC
3801	TTTCCGTTCA	AGATGAATTG	GATCGTCTTT	TTGTAGATCA	AGCACAACTCT
3851	GCCGTGTGGA	CAAATATCGC	ACAGGATAAA	AGACGCTATG	ATTCTGATGC
3901	GTTCCGTGCT	TATCAGCAGA	AAACGAACTT	GCGTCAAATT	GGGGTGCAAA
3951	AAGCCTTAGA	TAATGGACGA	ATTGGGGCGG	TTTTCTCGCA	TAGCCGTTCA
4001	GATAATACCT	TTGACGAACA	GGTTAAAAAT	CACGCGACAT	TAGCGATGAT
4051	GTCGGGTTTT	GCCCAATATC	AATGGGGCGA	TTTACAATTT	GGTGTAAACG
4101	TGGGTGCGGG	AATTAGTGCG	AGTAAATGG	CTGAAGAACA	AAGCCGAAAA
4151	ATTCATCGAA	AAGCGATAAA	TTATGGTGTG	AATGCAAGTT	ATCAGTTCGG
4201	TTTAGGGCAA	TTGGGTATTC	AGCCTTATTT	GGGTGTTAAT	CGATATTTTA

Fig. 18B

4251 TTGAACGTGA AAATTATCAA TCTGAAGAAG TGAAAGTGCA AACACCGAGC  
4301 CTTGTATTTA ATCGCTATAA TGCTGGCATT CGAGTTGATT ATACATTTAC  
4351 CCCGACAGAT AATATCAGCA TTAAGCCTTA TTTCTTCGTC AATTATGTTG  
4401 ATGTTTCAAA CGCTAACGTA CAAACCACTG TAAATCGCAC GATGTTGCAA  
4451 CAATCATTTG GGCGTTATTG GCAAAAAGAA GTGGGATTAA AGGCAGAAAT  
4501 TTTACATTTT CAACTTTCCG CTTTTATCTC AAAATCTCAA GGTTCAACAAC  
4551 TCGGCAAACA GCAAAATGTG GCGGTGAAAT TGGGGTATCG TTGGTAAAAA  
4601 TCAAC

Fig. 18C

Amino acid sequence for NTHi strain TN106 Hap protein (first amino acid to last amino acid):

```

1  MKKTVFRLNF LTACISLGIV SQAWAGHTYF GIDYQYYRDF AENKGKFTVG
51  AQDIDIYNKK GEMIGTMMKG VPMPDLSSMV RGGYSTLISE QHLISVAHNV
101 GYDVVDFGME GENPDQHRFK YKVVKRYNYK SGDRQYNDYQ HPRLEKFBVTE
151 TAPIEMVSYM DGNHYKNFNQ YPLRVRVGSG HQWWKDDNNK TIGDLAYGGS
201 WLIGGNTFED GPAGNGTLEL NGRVQNPKNY GPLPTAGSFG DSGSPMFIYD
251 KEVKKWLLNG VLREGNPYAA VGNSYQITRK DYFQGILNQD ITANFWDTNA
301 EYRFNIGSDH NGRVATIKST LPKKAIQPER IVGLYDNSQL HDARDKNGDE
351 SPSYKGPNPW SPALHHGKSI YFGDQGTGTL TIENNINQGA GGLYFEGNFV
401 VKGNQNNITW QGAGVSVGEE STVEWQVHNP EGDRLSKIGL GTLLVNGKKG
451 NLGSLSVGNG LVLVDQQADE SGQKQAFKEV GIVSGRATVQ LNSADQVDPN
501 NIYFGFRGGR LDLNGHSLTF ERIQNTDEGA MIVNHNASQT ANITITGNAT
551 INSDSKQLTN KKDIAFNGWF GEQDKAKTNG RLNVNYQPVN AENHLLLSGG
601 TNLNGNITQN GGTLVFSGRP TPHAYNHLRR DLSNMEGIPQ GEIVWDHDWI
651 NRTFKAENFQ IKGGSASVSR NVSSIEGNWT VSNANATFG VVPNQQNTIC
701 TRSDWTGLTT CKTVDLTDKK VINSIPTTQI NGSINLTDNA TVNIHGLAKL
751 NGNVTLIDHS QFTLSNNATQ TGNIKLSNHA NATVDNANLN GNVNLMDSAQ
801 FSLKNSHFSH QIQGGEDTTV MLENATWTMP SDTTLQNLTL NNSTVTLNSA
851 YSAISNNAPR RRRRSLETET TPTSAEHRFN TLTVNGKLSG QGTFQFTSSL
901 FGYKSDKLKL SNDAEGDYTL SVRNTGKEPV TFGQLTLVES KDNKPLSDKL
951 TFTLENDHVD AGALRYKLVK NDGEFRLHNP IKEQELRSDL VRAEQAERTL
1001 EAKQVEQTAK QTTSKARVRS RRAVFSDDLQ AQSLKALEA KQALTTETQT
1051 SKAKKVRSKR AAREFSDTLP DQILQAALV IDAQQQVKKE PQTQEEEEKR
1101 QRKQKELISR YSNSALSELS ATVNSMLSVQ DELDRLFVDQ AQSASVTNIA
1151 QDKRRYSDA FRAYQQKTNL RQIGVQKALD NGRIGAVFSH SRSDNTFDEQ
1201 VKNHATLMM SGFAQYQWGD LQFGVNVGAG ISASKMAEEQ SRKIHRKAIN
1251 YGVNASYQFR LGQLGIQPYL GVNRYFIERE NYQSEEVKVQ TPSLVFNRYN
1301 AGIRVDYFTT PTDNISIKPY FFVNYVDVSN ANVQTTVNRT MLQQSFGRYW
1351 QKEVGLKAEI LHFQLSAFIS KSQGSQLGKQ QNVGVKLGYS W

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Fig. 19

Nucleotide sequence for NTHi strain 860295 *hap* gene (start codon begins at position 430, stop codon begins at position 4738):

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1  GGAGGCAGTG GTGGCGGACA AATTATTGCG ACGGGTACGC CAGAACAAGT
51  TGCCAAAGTA GAAAGTTCCC ACACCGCCCG CTTCTTAAA CCGATTTTAG
101 AAAAACCTTA GAAAAAATGA CCGCACTTTC AGAGAAAAC CACATAAAGT
151 GCGGTTATTT TATTAGTGAT ATTGTTTTAA TTTTAGTTAT CTGTATAAAT
201 TACATATAAT ATTAATCCAT CGCAAGATAA GATTACCCAC TAAGTATTAA
251 GCAAAAACCT AGAAATTTTG GCTTAATTAC TATATAGTTT TACTGCTTTA
301 TTTTCTTTTG TGCCTTTTAG TTCGTTTTTT TAGCTGAAAT CCCTTAGAAA
351 ATCACCGCAC TTTTATTGTT CAATAGTCGT TTAACCACGT ATTTTTTAAT
401 ACGAAAAATT ACTTAATTAA ATAAACATTA TGAAAAAAC TGTATTTTCGT
451 CTGAACTTTT TAACCGCTTG CATTTCATTA GGGATAGTAT CGCAAGCGTG
501 GGCAGGTCAC ACTTATTTTG GGATTGACTA CCAATATTAT CGTGATTTTG
551 CTGAGAATAA AGGGAAGTTT TCAGTTGGGG CTAAAAATAT TGAGGTTTAT
601 AACAAAGAGG GGACTTTAGT TGGCACATCA ATGACAAAAG CCCCGATGAT
651 TGATTTTTCT GTGGTGTTCG GAAATGGGGT GCGGCATTA GTAGGCGATC
701 AGTATATTGT GAGTGTGGCA CATAACGGTG GATATAATAG CGTTGATTTT
751 GGAGCAGAAG GTCCAAATCC CGATCAGCAT CGTTTTACTT ATCAAATTGT
801 AAAAAGAAAT AATTATAAGC CAGGCAAAGA TAACCCTTAT CATGGTGACT
851 ATCACATGCC TCGTTTGCAC AAATTTGTCA CTGACGCTGA ACCAGCAAAG
901 ATGACAGACA ATATGAATGG AAAGAACTAC GCTGATTTAA GTAAATATCC
951 TGATCGTGTG CGTATTGGTA CAGGTGAACA ATGGTGAGG ACTGATGAAG
1001 AACAAAAGCA AGGAAGTAAG AGTTCATGGC TTGCTGATGC TTATCTGTGG
1051 AGAATAGCAG GTAACACACA TTCACAAAGT GGAGCGGGCA ACGGCACGGT
1101 AAACCTAAGT GGAGATATCA CAAAACCAA TAACCTATGA CCTCTTCCTA
1151 CGGGTGTTC GTTTGGAGAT AGTGGTTCCT CAATGTTTAT TTATGATGCA
1201 ATAAAACAAA AATGGCTTAT TAATGGCGTA TTGCAAACTG GTAACCCTTT
1251 CTCGGGAGCT GGAAATGGAT TCCAATTAAT TAGAAAAAAT TGGTTTTATG
1301 ATAATGTCTT TGTAGAAGAT TTGCCTATAA CATTTTTAGA GCCAAGAAGT
1351 AACGGTCATT ATTCATTTAC TTCAAATAAT AATGGAAGT GTACGGTTAC
1401 TCAAACGAAT GAAAAAGTGA GTATGCCTCA ATTTAAAGTC AGAACGGTTC
1451 AGTTATTTAA TGAAGCATTA AAAGAAAAAG ATAAAGAACC TGTTTATGCT
1501 GCAGGTGGTG TAAATGCTTA TAAACCAAGA CTAAATAATG GTAAAAATAT
1551 TTACTTTGGC GATCGAGGAA CAGGAACTTT AACAATTGAA AATAATATAA
1601 ATCAAGGTGC TGGTGGTTTG TATTTTGAGG GTAACTTTAC GGTATCTTCA
1651 GAAAATAATG CAACTTGGCA AGGTGCTGGA GTGCATGTAG GTGAAGACAG
1701 TACTGTTACT TGGAAAGTAA ACGGCGTGGA ACATGATCGC CTTTCTAAAA
1751 TTGGTAAAGG AACGTTGCAT ATTCAAGCAA AAGGTGAAAA CTTAGGCTCA
1801 ATTAGCGTAG GTGACGGCAA AGTCATTTTA GATCAACAAG CCGATGAGAA
1851 CAACCAAAAA CAAGCCTTTA AAGAAGTTGG CATTGTAAGT GGTAGAGCTA
1901 CCGTTCAACT AAATAGTGCA GATCAAGTTG ATCCTAACAA TATTTATTTT
1951 GGATTTTCGT GTGGTCGCTT AGATCTTAAC GGACATTCAT TAACCTTTAA
2001 ACGTATCCAA AATACGGACG AGGCGCGGAT GATTGTGAAC CATAATACAA

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Fig. 20A

2051	CTCAAGTCGC	TAATATTACT	ATTACTGGGA	ACGAAAGTAT	TACTGCTCCA
2101	TCTAATAAAA	ATAATATTAA	TAAACTTGAT	TACAGCAAAG	AAATTGCTTA
2151	CAACGGTTGG	TTTGGCGAAA	CAGATGAAAA	TAAACACAAT	GGAAGATTAA
2201	ACCTTATTTA	TAAACCAACC	ACAGAAGATC	GTACTTTGCT	ACTTTCAGGT
2251	GGAACAAATT	TAAAAGGCAA	TATTACTCAG	GAAGGCGGCA	CTTTAGTGTT
2301	TAGTGGTCGC	CCAACTCCAC	ACGCTTACAA	TCATTTAAAT	CGCCCAAACG
2351	AGCTTGGGCG	ACCTCAAGGC	GAAGTGGTTA	TTGATGACGA	TTGGATCACC
2401	CGCACATTTA	AAGCTGAAAA	CTTCCAAATT	AAAGGCGGAA	GTGCGGTGGT
2451	TTCTCGCAAT	GTTTCTTCAA	TTGAGGGAAA	TTGGACAGTC	AGCAATAATG
2501	CAAATGCCGC	ATTTGGTGTT	GTGCCAAATC	AGCAAATAC	CATTTGCACG
2551	CGTTCAGATT	GGACAGGATT	AACGACTTGT	AAAACGTGG	ATTTAACCGA
2601	TACAAAAGTT	ATTAATTCCA	TACCGACAAC	ACAAATTAAT	GGCTCTATTA
2651	ATTTAACTGA	TAATGCAACA	GTGAATATTC	ATGGTTTAGC	AAAACCTAAT
2701	GGTAATGTCA	CTTTAATAAA	TCATAGCCAA	TTTACATTGA	GCAACAATGC
2751	CACCCAAACA	GGCAATATCC	AACTTTCAAA	TCACGCAAAT	GCAACGGTGG
2801	ACAATGCAAA	TTTGAACGGT	AATGTGCATT	TAACGGATTTC	TGCTCAATTT
2851	TCTTTAAAAA	ACAGCCATTT	TTCGCACCAA	ATTCAGGGCG	ACAAAGACAC
2901	AACAGTGACG	TTGGAAAATG	CGACTTGGAC	AATGCCTAGC	GATGCCACAT
2951	TGCAGAATTT	AACGCTAAAT	AATAGTACTG	TTACGTTAAA	TTCAGCTTAT
3001	TCAGCTAGCT	CAAATAATGC	GCCACGTCAC	CGCCGTTTCAT	TAGAGACGGA
3051	AACAACGCCA	ACATCGGCAG	AACATCGTTT	CAACACATTG	ACAGTAAATG
3101	GTAAATTGAG	CGGGCAAGGC	ACATTCCAAT	TTACTTCATC	TTTATTTGGC
3151	TATAAAAGCG	ATAAATTAAA	ATTATCCAAT	GACGCTGAGG	GCGATTACAC
3201	ATTATCTGTT	CGCAACACAG	GCAAAGAACC	CGAAGCCCTT	GAGCAATTAA
3251	CTTTGGTTGA	AAGCAAAGAT	AATAAACCGT	TATCAGACAA	ACTCAAATTT
3301	ACTTTAGAAA	ATGACCACGT	TGATGCAGGT	GCATTACGTT	ATAAATTAGT
3351	GAAGAATAAT	GGCGAATTCC	GCTTGCATAA	CCCAATAAAA	GAGCAGGAAT
3401	TGCGCAATGA	TTTAGTAAGA	GCAGAGCAAG	CAGAACGAAC	ATTAGAAGCC
3451	AAACAAGTTG	AACAGACTGC	TGAAACACAA	ACAAGTAATG	CAAGAGTGCG
3501	GTCAAAAAGA	GCGGTGTTTT	CTGATACCC	GCCTGATCAA	AGCCAGTTAG
3551	ACGTATTACA	AGCCGAACAA	GTTGAACCGA	CTGCTGAAAA	ACAAAAAAT
3601	AAGGCAAAAA	AAGTGCGGTC	AAAAAGAGCG	GTGTTTTCTG	ATACCCTGCC
3651	TGATCAAAGC	CAGTTAGACG	TATTACAAGC	CGAACAAGTT	GAACCGACTG
3701	CTGAAAAACA	AAAAAATAAG	GCAAAAAAAG	TGCGGTCAAA	AAGAGCCGCG
3751	AGAGAGTTTT	CTGATACCCC	GCTTGATCTA	AGCCGGTTAA	AGGTATTAGA
3801	AGTCAAACCT	GAGGTTATTA	ATGCCCAACA	GCAAGTGAAA	AAAGAACCTC
3851	AAGATCAAGA	GAAACAACGC	AAACAAAAAG	ACTTGATCAG	CCGTTATTCA
3901	AATAGTGCGT	TATCAGAATT	ATCTGCAACA	GTAAATAGTA	TGCTTTCTGT
3951	TCAAGATGAA	TTAGATCGTC	TTTTTGTAGA	TCAAGCACAA	TCTGCCGTGT
4001	GGACAAATAT	CGCACAGGAT	AAAAGACGCT	ATGATTCTGA	TGCGTTCCGT
4051	GCTTATCAGC	AGAAAACGAA	CTTACGTCAA	ATTGGGGTGC	AAAAAGCCTT
4101	AGCTAATGGA	CGAATTGGGG	CAGTTTTCTC	GCATAGCCGT	TCAGATAATA
4151	CTTTTGATGA	ACAGGTTAAA	AATCACGCGA	CATTAACGAT	GATGTCGGGT
4201	TTTGCCCAAT	ATCAATGGGG	CGATTTACAA	TTTGGTGTA	ACGTGGGAAC

Fig. 20B

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4251  GGAATCAGT  GCGAGTAAAA  TGGCTGAAGA  ACAAAGCCGA  AAAATTCATC
4301  GAAAAGCGAT  AAATTATGGC  GTGAATGCAA  GTTATCAGTT  CCGTTTAGGG
4351  CAATTGGGCA  TTCAGCCTTA  TTTTGGAGTT  AATCGCTATT  TTATTGAACG
4401  TGAAAATTAT  CAATCTGAGG  AAGTGAAAGT  GAAAACGCCT  AGCCTTG CAT
4451  TTAATCGCTA  TAATGCTGGC  ATTCGAGTTG  ATTATACATT  TACTCCGACA
4501  GATAATATCA  GCGTTAAGCC  TTATTTCTTC  GTCAATTATG  TTGATGTTTC
4551  AAACGCTAAC  GTACAAACCA  CGGTAAATAG  CACGGTGTTG  CAACAACCAT
4601  TTGGACGTTA  TTGGCAAAAA  GAAGTGGGAT  TAAAAGCGGA  AATTTTACAT
4651  TTCCAAC TTT  CTGCTTTTAT  TTCTAAATCT  CAAGGTTTCGC  AACTCGGCAA
4701  ACAGCAAAAT  GTGGGCGTGA  AATTGGGGTA  TCGTTGGTAA  AAATCAACAT
4751  AATTGTATCG  TTTATTGATA  AACAAGGTGG  GGCAGATCCC  ACCTTTTTTA
4801  TTTCAATAAT  GGAAC TTTAT  TTAATTAAGA  GCATCTAAGT  AGCACCCCAT
4851  ATAGGGGATT  AATTAAGAGG  ATTTAATAAT  GAATTTA ACT  AAAC TTTTAC
4901  CAGCATTTGC  TGCTGCAGTC  GTATTATCTG  CTTGTGCAAA  GGATGCACCT
4951  GAAATGACAA  AATCATCTGC  GCAAATAGCT  GAAATGCAAA  CACTTCCAAC
5001  AATCACTGAT  AAAACAGTTG  TATATTCCTG  CAATAAACAA  ACTGTA ACTG
5051  CCGTGTATCA  ATTTGAAAAC  CAAGAACCAG  TTGCTGCAAT  GGTAAGTGTG
5101  GGCGATGGCA  TTATTGCGAA  AGATTTTACT  CGTGATAAAT  CACAAAATGA
5151  CTTTACAAGT  TTCGTTTCTG  GGGATTATGT  TTGGAATGTA  GATAGTGGCT
5201  TAACGTTAGA  TAAATTTGAT  TCTGTTGTGC  CTGTCAATTT  AATTC

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Fig. 20C

Amino acid sequence for NTHi strain 860295 Hap protein (first amino acid to last amino acid):

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 1  MKKTVFRLNF LTACISLGIV SQAWAGHTYF GIDYQYYRDF AENKGKFSVG
51  AKNIEVYNKE GTLVGTSMTK APMIDFSVVS RNGVAALVGD QYIVSVAHNG
101 GYNSVDFGAE GPNPDQHRFT YQIVKRNNYK PGKDNPHYGD YHMPRLHKFV
151 TDAEPAKMTD NMNGKNYADL SKYPDRVRIG TGEQWWRTDE EQKQGSKSSW
201 LADAYLWRIA GNTHSQSGAG NGTVNLSGDI TKPNNYGPLP TGVSFGDSGS
251 PMFIYDAIKQ KWLINGVLQT GNPFSGAGNG FQLIRKNWFY DNVFVEDLPI
301 TFLEPRSNHG YSFTSNNGGT GTVTQTNEKV SMPQFKVRTV QLFNEALKEK
351 DKEPVYAAGG VNAYKPRLNN GKNIFYGDRG TGTTLTIENNI NQGAGGLYFE
401 GNFTVSSENN ATWQGAGVHV GEDSTVTWKV NGVEHDRLSK IGKGTLHIQA
451 KGENLGSISV GDGKVILDQQ ADENNQKQAF KEVGIVSGRA TVQLNSADQV
501 DPNNIYFGFR GGRLDLNGHS LTFKRIQNTD EGAMIVNHNT TQVANITITG
551 NESITAPSNK NNINKLDYSK EIAYNWGFGE TDENKHNGRL NLIYKPTTED
601 RTLLLSGGTN LKGNITQEGG TLVFSGRPTP HAYNHLNRPN ELGRPQGEVV
651 IDDDWITRTF KAENFQIKGG SAVVSRNVSS IEGNWTVSNN ANAAFVGVPN
701 QQNTICTRSD WTGLTTCKTV DLTDTKVINS IPTTQINGSI NLTDNATVNI
751 HGLAKLNGNV TLINHSQFTL SNNATQTGNI QLSNHANATV DNANLNGNVH
801 LTDSAQFSLK NSHFSHQIQG DKDTTVTLEN ATWTMPSDAT LQNLTLNNST
851 VTLNSAYSAS SNNAPRHRRS LETETTP TSA EHRFNTLTVN GKLSGQGTFO
901 FTSSLFGYKS DKLKLSNDAE GDYTLVRNT GKEPEALEQL TLVESKDNKP
951 LSDKLKFTLE NDHVDAGALR YKLVKNNGEF RLHNPIKEQE LRNDLVRAEQ
1001 AERTLEAKQV EQTAETQTSN ARVRSKRAVF SDTLPDQSQL DVLOAEQVEP
1051 TAEKQKNKAK KVRSKRAVFS DTLPDQSQLD VLQAEQVEPT AEKQKNKAKK
1101 VRSKRAAREF SDTPLDL SRL KVLEVKLEVI NAQQQVKKEP QDQEKQRKQK
1151 DLISRYSNSA LSELSATVNS MLSVQDELDL LFVDQAQSAV WTNIAQDKRR
1201 YDSDAFRAYQ QKTNLRQIGV QKALANGRIG AVFSHSRSDN TFDEQVKNHA
1251 TLTMMSGFAQ YQWGD LQFGV NVGTGISASK MAEEQSRKIH RKAINYG VNA
1301 SYQFRLGQLG IQPYFGV NRY FIERENYQSE EVKVKT PSLA FNRYNAGIRV
1351 DYTFTPTDNI SVKPYFFVNY VDVSNANVQT TVNSTVLQQP FGRYWQKEVG
1401 LKAEILHFQL SAFISKSQGS QL GKQQNVGV KLG YRW

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Fig. 21

Nucleotide sequence for NTHi strain 3219B *hap* gene (start codon begins at position 388, stop codon begins at position 4561):

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1   CCTGAAGACG TTGCTCAAGT TAAAGGCTCT CACACAGCCC GATTCCTTAA
51  ACCGATTTTA GAAAAACCTT AGAAAAAATG ACCGCACTTT CAGAGAAAAAC
101 TCACATAAAG TGCGGTTATT TTATTAGTGA TATTGTTTTA ATTATTTGTA
151 TAAATTACAT ACAATATTAA TCCATCGAAA AATAAGATTA CCCACTAAGT
201 ATTAAGCCAA AACCTAGAAA TTTTGGCTTA ATTACTATAT AATTTTACTC
251 CTTTATTTTC TTTTGTGCCT TTTAGTTAGT TCGTTTTTTA GCTGAAATCC
301 CTCAGAAAAT CACCGCACTT TTATTGTTCA ATAGTCGTTT AACCACGTAT
351 TTTTAAATAC GAAAAATTAC TTAATTAAAT AAACATTATG AAAAAAACTG
401 TATTTTCGCT TAATTTTCTA ACCGCTTGTA TTTCATTAGG GATAGTATCG
451 CAAGCGTGGG CAGGTCACAC TTATTTTGGG ATTGACTACC AATATTATCG
501 TGATTTTGCC GAGAATAAAG GGAAGTTTAC AGTTGGGGCT CAAGATATTG
551 ATATCTACAA TAAAAAAGGG GAAATGATAG GTACGATGAT GAAAGGTGTG
601 CCTATGCCTG ATTTATCTTC CATGGTTCGT GGTGGTTATT CAACATTGAT
651 AAGTGAGCAG CATTTAATTA GCGTCGCACA TAATGTAGGG TATGATGTCTG
701 TTGATTTTGG TATGGAGGGG GAAATCCAG ACCAACATCG TTTTAAGTAT
751 AAAGTTGTTA AACGATATAA TTATAAGAGC GGTGATAGAC AATATAATGA
801 TTATCAACAT CCAAGATTAG AGAAATTTGT AACGGAAACT GCACCTATTG
851 AAATGGTTTC ATATATGGAT GGTAATCATT ACAAAAATTT TAATCAATAT
901 CCTTTGCGAG TTAGAGTTGG AAGTGGGCAT CAATGGTGGG AAGACGATAA
951 TAATAAAACC ATTGAGACT TAGCCTATGG AGGTTTCATGG TTAATAGGTG
1001 GAAATACCTT TGAAGATGGA CCAGCTGGTA ACGGTACATT AGAATTAAAT
1051 GGGCGAGTAC AAAATCCTAA TAAATATGGT CCACTACCTA CGGCAGGTTC
1101 ATTCGGGGAT AGTGGTTCCTC CAATGTTTAT TTATGATAAG GAAGTTAAGA
1151 AATGGTTATT AAATGGCGTG TTACGTGAAG GAAATCCTTA TGCTGCAGTA
1201 GGAAACAGCT ATCAAATTAC ACGAAAAGAT TATTTTCAAG GTATTCTTAA
1251 TCAAGACATT ACAGCTAATT TTTGGGATAC TAATGCTGAA TATAGATTTA
1301 ATATAGGGAG TGACCACAAT GGAAGAGTGG CAACAATCAA AAGTACATTA
1351 CCTAAAAAAG CTATTCAGCC TGAACGAATA GTGGGTCTTT ATGATAATAG
1401 CCAACTTCAT GATGCTAGAG ATAAAAATGG CGATGAATCT CCCTCTTATA
1451 AAGGTCCTAA TCCATGGTCG CCAGCATTAC ATCATGGGAA AAGTATTTAC
1501 TTTGGCGATC AAGGAACAGG AACTTTAACA ATTGAAAATA ATATAAATCA
1551 AGGTGCAGGT GGATTGTATT TTGAAGGTAA TTTTGTTGTA AAAGGCAATC
1601 AAAATAATAT AACTTGGCAA GGTGCAGGCG TTTCTGTTGG AGAAGAAAGT
1651 ACTGTTGAAT GGCAGGTGCA TAATCCAGAA GGCGATCGCT TATCCAAAAT
1701 TGGGCTGGGA ACCTTACTTG TTAATGGTAA AGGGAAAAAC TTAGGAAGCC
1751 TGAGTGTCTG TAACGGTTTG GTTGTGTTAG ATCAACAAGC AGATGAATCA
1801 GGTCAAAAAC AAGCCTTTAA AGAAGTTGGC ATTGTAAGTG GTAGAGCTAC
1851 CGTTCAACTA AATAGTGCAG ATCAAGTTGA TCCTAACAAT ATTTATTTCTG
1901 GCTTTCGTGG TGGTCGCTTA GATCTTAATG GGCATTCATT AACCTTTGAA
1951 CGTATCCAAA ATACGGATGA AGGCGCGATG ATTGTGAACC ACAACGCTTC
2001 TCAAACCGCA AATATTACGA TTACAGGCAA CGCAACTATT AATTCAGATA

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Fig. 22A



2051	GCAAACAAC	TACTAATAAA	AAAGATATTG	CATTTAACGG	CTGGTTTGGT
2101	GAGCAAGATA	AAGCTAAAAC	AAATGGTCGT	TTAAATGTGA	ATTATCAACC
2151	AGTTAATGCA	GAAAATCATT	TGTTGCTTTC	TGGGGGGACA	AATTTAAACG
2201	GCAATATCAC	GCAAAATGGT	GGTACGTTAG	TTTTTAGTGG	TCGTCCAACG
2251	CCTCATGCTT	ACAATCATTT	AAGAAGAGAC	TTGTCTAACA	TGGAAGGTAT
2301	CCCACAAGGC	GAAATTGTGT	GGGATCACGA	TTGGATCAAC	CGCACATTTA
2351	AAGCTGAAAA	CTTCCAAATT	AAAGGCGGAA	GTGCGGTGGT	TTCTCGCAAT
2401	GTTTCTTCAA	TTGAGGGAAA	TTGGACAGTC	AGCAATAATG	CAAATGCCAC
2451	ATTTGGTGT	GTGCCAAATC	AGCAAAATAC	CATTTGCACG	CGTTCAGATT
2501	GGACAGGATT	AACGACTTGT	AAAACAGTTG	ATTTAACCGA	TAAAAAAGTT
2551	ATTAATTCCA	TACCGACAAC	ACAAATTAAT	GGTCTATTA	ATTTAACTGA
2601	TAATGCAACA	GTGAATATTC	ATGGTTTAGC	AAAACCTAAT	GGTAATGTCA
2651	CTTTAATAGA	TCACAGCCAA	TTTACATTGA	GCAACAATGC	CACCCAAGCA
2701	GGCAATATCA	AACTTTCAAA	TCACGCAAAT	GCAACGGTGG	ACAATGCAAA
2751	TTTGAACGGT	AATGTGAATT	TAATGGATT	TGCTCAATTT	TCTTTAAAAA
2801	ACAGCCATTT	TTCGCACCAA	ATCCAAGGTG	GGGAAGACAC	AACAGTGATG
2851	TTGGAAAATG	CGACTTGGAC	AATGCCTAGC	GATACCACAT	TGCAGAAATTT
2901	AACGCTAAAT	AATAGTACTG	TTACGTTAAA	TTCAGCTTAT	TCAGCTATCT
2951	CAAATAATGC	GCCACGCCGT	CGCCGCCGTT	CATTAGAGAC	GGAAACAACG
3001	CCAACATCGG	CAGAACATCG	TTTCAACACA	TTGACAGTAA	ATGGTAAATT
3051	GAGCGGGCAA	GGCACATTCC	AATTTACTTC	ATCTTTATTT	GGCTATAAAA
3101	GCGATAAATT	AAAATTATCC	AATGACGCTG	AGGGCGATTA	CACATTATCT
3151	GTTTCGCAACA	CAGGCAAAGA	ACCCGTGACC	TTTGGGCAAT	TAACTTTGGT
3201	TGAAAGCAAA	GATAATAAAC	CGTTATCAGA	CAAACCTACA	TTACGTTAG
3251	AAAATGACCA	CGTTGATGCA	GGTGCATTAC	GTTATAAATT	AGTGAAGAAT
3301	GATGGCGAAT	TCCGCTTACA	TAACCCAATA	AAAGAGCAGG	AATTGCGCTC
3351	TGATTTAGTA	AGAGCAGAGC	AAGCAGAACG	AACATTAGAA	GCCAAACAAG
3401	TTGAACAGAC	TGCTAAAACA	CAAACAAGTA	AGGCAAGAGT	GCGGTCAAGA
3451	AGAGCGGTGT	TTTCTGATCC	CCTGCCTGCT	CAAAGCCTGT	TAAACGCATT
3501	AGAAGCCAAA	CAAGCTCTGA	CTACTGAAAC	ACAAACAAGT	AAGGCCAAAA
3551	AAGTGCGGTC	AAAAAGAGCT	GCGAGAGAGT	TTTCTGATAC	CCTGCCTGAT
3601	CAAATATTAC	AAGCCGCACT	TGAGGTTATT	GATGCCCAAC	AGCAAGTGAA
3651	AAAAGAACCT	CAAACCTCAAG	AGGAAGAAGA	GAAAAGACAA	CGCAAACAAA
3701	AAGAATTGAT	CAGCCGTTAC	TCAAATAGTG	CGTTATCGGA	GTTGTCTGCG
3751	ACAGTAAATA	GTATGCTTTC	CGTTCAAGAT	GAATTGGATC	GTCTTTTGT
3801	AGATCAAGCA	CAATCTGCCG	TGTGGACAAA	TATCGCACAG	GATAAAAGAC
3851	GCTATGATT	TGATGCGTTC	CGTGCTTATC	AGCAGAAAAC	GAACCTTGCCT
3901	CAAATTGGGG	TGCAAAAAGC	CTTAGATAAT	GGACGAATTG	GGGCGGTTTT
3951	CTCGCATAGC	CGTTCAGATA	ATACCTTTGA	CGAACAGGTT	AAAAATCACG
4001	CGACATTAGC	GATGATGTCT	GGTTTTGCCC	AATATCAATG	GGGCGATTTA
4051	CAATTTGGTG	TAAACGTGGG	TGCGGGAATT	AGTGCGAGTA	AAATGGCTGA
4101	AGAACAAAGC	CGAAAAATTC	ATCGAAAAGC	GATAAATTAT	GGTGTGAATG
4151	CAAGTTATCA	GTTCCGTTTA	GGGCAATTGG	GTATTCAGCC	TTATTTGGGT
4201	GTTAATCGAT	ATTTTATTGA	ACGTGAAAAT	TATCAATCTG	AAGAAGTGAA

Fig. 22B

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4251 AGTGCAAACA CCGAGCCTTG TATTTAATCG CTATAATGCT GGCATTTCGAG
4301 TTGATTATAC ATTTACCCCG ACAGATAATA TCAGCATTAA GCCTTATTTC
4351 TTCGTCAATT ATGTTGATGT TTCAAACGCT AACGTACAAA CCACTGTAAA
4401 TCGCACGATG TTGCAACAAT CATTTGGGCG TTATTGGCAA AAAGAAGTGG
4451 GATTAAAGGC AGAAATTTTA CATTTCCAAC TTTCCGCTTT TATCTCAAAA
4501 TCTCAAGGTT CACAACTCGG CAAACAGCAA AATGTGGGCG TGAAATTGGG
4551 GTATCGTTGG TAAAAATCAA CATAATTTTA TCGTTTATTG ATAAACAAGG
4601 TGGGGCAGAT CAAATCCTAC CTTTTTTTATT CCAATAATGG AACTTTATTT
4651 TATTAAAGGT ATCTAAGTAG CACCCTATAT AGGGATTAAT TAAGAGGATT
4701 TAATAATGAA TTTAACATAA ATTTTACCCA CATTTGCTGC TGTAGTCGTA
4751 TTATCTGCTT GTGCAAAGGA TGCACCTGAA ATGACAAAAT CATCTGCGCA
4801 AATAGCTGAA ATGCAAACAC TT

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Fig. 22C

Amino acid sequence for NTHi strain 3219B Hap protein (first amino acid to last amino acid):

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1  MKKTVFRLNF LTACISLGIV SQAWAGHTYF GIDYQYYRDF AENKGKFTVG
51  AQDIDIYNKK GEMIGTMMKG VPMPDLSSMV RGGYSTLISE QHLISVAHNV
101 GYDVVDFGME GENPDQHRFK YKVVKRYNYK SGDRQYNDYQ HPRLEKFVTE
151 TAPIEMVSYM DGNHYKNFNQ YPLRVRVGSG HQWWKDDNNK TIGDLAYGGS
201 WLIGGNTFED GPAGNGTLEL NGRVQNPKNKY GPLPTAGSFG DSGSPMFIYD
251 KEVKKWLLNG VLREGNPYAA VGNSYQITRK DYFQGILNQD ITANFWDTNA
301 EYRFNIGSDH NGRVATIKST LPKKAIQPER IVGLYDNSQL HDARDKNGDE
351 SPSYKGPNPW SPALHHGKSI YFGDQGTGTL TIENNINQGA GGLYFEGNFV
401 VKGNQNNITW QGAGVSVGEE STVEWQVHNP EGDRLSKIGL GTLLVNGKKG
451 NLGSLSVGNG LVVLDQQADE SGQKQAFKEV GIVSGRATVQ LNSADQVDPN
501 NIYFGFRGGR LDLNGHSLTF ERIQNTDEGA MIVNHNASQT ANITITGNAT
551 INSDSKQLTN KKDI AFNGWF GEQDKAKTNG RLNVNYQPVN AENHLLLSGG
601 TNLNGNITQN GGTLVFSGRP TPHAYNHLRR DLSNMEGIPQ GEIVWDHDWI
651 NRTFKAENFQ IKGGS AVVSR NVSSIEGNWT VSNNANATFG VVPNQONTIC
701 TRSDWTGLTT CKTVDLTDKK VINSIPTTQI NGSINLTDNA TVNIHGLAKL
751 NGNVTLIDHS QFTLSNNATQ AGNIKLSNHA NATVDNANLN GNVNLMDSAQ
801 FSLKNSHFSH QIQGGEDTTV MLENATWTMP SDTTLQNLTL NNSTVTLNSA
851 YSAISNNAPR RRRRSLETET TPTSAEHRFN TLTVNGKLSG QGTFQFTSSL
901 FGYKSDKLKL SDAEGDYTL SVRNTGKEPV TFGQLTLVES KDNKPLSDKL
951 TFTLENDHVD AGALRYKLVK NDGEFRLHNP IKEQELRSDL VRAEQAERTL
1001 EAKQVEQTAK TQTSKARVRS RRAVFS DPLP AQSLNNALEA KQALTTETQT
1051 SKAKKVRSKR AAREFS DTL P DQILQA ALEV IDAQQQVKKE PQTQEEEEKR
1101 QRKQKELISR YSNSALS ELS ATVNSMLS VQ DELDRL FVDQ AQSAVWTNIA
1151 QDKRRYSDA FRAYQQ KTNL RQIGVQ KALD NGRIGAVFSH SRSDNTFDEQ
1201 VKNHATLAMM SGFAQYQWGD LQFGVNVGAG ISASKMAEEQ SRKIHRKAIN
1251 YGVNASYQFR LGQLGIQPYL GVNRYFIERE NYQSEEVKVQ TPSLVFNRYN
1301 AGIRVDYTFT PTDNISIKPY FVNYVDVSN ANVQTTVNRT MLQQSFGRYW
1351 QKEVGLKAEI LHFQLSAFIS KSQGSQ LGKQ QNVGVKLG YR W

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Fig. 23

Nucleotide sequence for NTHi strain 1396B *hap* gene (start codon begins at position 313, stop codon begins at position 4546):

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1  TGACCGCACT TTCAGAGAAA ACTCACATAA AGTGCGGTTA TTTTATTAGT
51  GATATTGTTT TAATTTTAGT TATCTGTATA AATTACATAC AATATTAATC
101 CATCGCAAGA TAAGATTACC CACTAAGTAT TAAGCAAAAA CCTAGAAATT
151 TTGGCTTAAT TACTATATAG TTTTACTCAT TTATTTTCTT TTGTGCCTTT
201 TAGTTCGTTT TTTTAGCTGA AATCCCTTAG AAAATCACCG CACTTTTATT
251 GTTCAATAGT CGTTTAACCA CGTATTTTTT AATACGAAAA ATTACTTAAT
301 TAAATAAACA TTATGAAAAA AACTGTATTT CGTCTGAATT TTTTAACCGC
351 TTGCATTTCA TTAGGGATAG TATCGCAAGC GTGGGCAGGT CATACTTATT
401 TTGGGATTGA CTACCAATAT TATCGTGATT TTGCCGAGAA TAAAGGGAAG
451 TTCACAGTTG GGGCTAAAAA TATTGAGGTT TACAATAAAA ATGGAAATTT
501 AGTTGGCACA TCAATGACAA AAGCCCCAAT GATTGATTTT TCCGTGGTGT
551 CGCGAAATGG GGTGGCGGCA TTGGTGGGCG ATCAGTATAT TGTGAGTGTG
601 GCACATAATG TAGGCTATAC CAATGTGGAT TTTGGTGCTG AAGGACAAAA
651 TCCTGATCAA CATCGTTTTA CTTATAAAAT TGTGAAACGG AATAATTATA
701 AAAACGATCA AACGCATCCT TATGAGAAAG ACTACCACAA CCCACGCTTA
751 CATAAATTTG TTACGGAAGC CACCCCAATC GATATGACTT CTGATATGAA
801 CGGCAACAAA TATACAGATA GGACGAAATA TCCCGAACGC GTGCGTATCG
851 GCTCCGGGTG GCAGTTTTGG CGAAACGATC AAAACAACGG CGACCAAGTT
901 GCCGGCGCAT ATCATTACCT GACAGCAGGC AATACACACA ACCAAGGCGG
951 AGCAGGGGGC GGCTGGTCAA GTCTGAGCGG CGATGTGCGC CAAGCGGGCA
1001 ATTACGGCCC CATTCTTATT GCAGGCTCAA GCGGCGACAG CGGTTTCGCT
1051 ATGTTTATTT ATGATGCGGA AAAACAAAAA TGGTTGATTA ACGGCGTATT
1101 GAGGACCGGC AACCTTGCGG CGGGGACAGA GAATACATTC CAACTGGTAC
1151 GCAAGTCTTT TTTTGATGAA ATCCTTGAAA AAGATTGCG TACATCGTTT
1201 TATAGCCCAT CGGGCAATGG TGCATACACC ATTACAGACA AAGGCGACGG
1251 CAGCGGCATT GTCAAACAAC AAACAGGAAG ACCATCTGAA GTCCGCATCG
1301 GTTTAAAGA CGACAAATTA CCTGCCGAAG GTAAAGACGA TGTTTACCAA
1351 TACCAAGGTC CAAATATATA CCTGCCTCGT TTGAATAACG GTGGAAACCT
1401 GTATTTCGGA GATCAAAAAA ACGGCACTGT TACCTTATCA ACCAACATCA
1451 ACCAAGGTGC GGGCGGTTTG TATTTTGAGG GTAACTTTAC GGTATCTTCA
1501 GAAAATAATG CAACTTGGCA AGGTGCTGGA GTGCATGTAG GTGAAGACAG
1551 TACTGTTACT TGGAAAGTAA ATGGTGTTGA AAATGATCGC CTTTCTAAAA
1601 TCGGCAAAGG CACATTGCAC GTTAAAGCCA AAGGGGAAAA TAAAGGTTTCG
1651 ATCAGCGTAG GCGATGGTAA AGTCATTTTG GAGCAGCAGG CAGACGATCA
1701 AGGCAACAAA CAAGCCTTTA GTGAAATTGG CTTGGTTAGT GGCAGAGGTA
1751 CGGTTCAAGT AAACGATGAC AAGCAATTTA ATACTGATAA ATTTTATTTT
1801 GGCTTCCGTG GTGGTCGCTT AGATCTTAAT GGGCATTTCAT TAACCTTTAA
1851 ACGTATCCAA AATACGGATG AGGGAGCAAC GATTGTTAAT CACAATGCCA
1901 CAACAGAATC TACAGTGACC ATTACTGGCA GCGATACCAT TAATGACAAC
1951 ACTGGCGATT TAACCAATAA ACGTGATATT GCTTTTAATG GTTGGTTTGG
2001 TGATAAAGAT GATACTAAAA ATACTGGACG TTTGAATGTT ACTTACAATC

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Fig. 24A

2051	CGCTTAACAA	AGATAATCAC	TTCCTTCTAT	CAGGTGGAAC	AAATTTAAAA
2101	GGCAATATTA	CTCAAGACGG	TGGCACTTTA	GTGTTTAGTG	GTCGCCCAAC
2151	ACCACACGCA	TACAATCATT	TAAATCGCCT	AAACGAGCTT	GGGCGACCTA
2201	AGGGCGAAGT	GGTTATTGAT	GACGATTGGA	TCAACCGTAC	ATTTAAAGCT
2251	GAAAACTTCC	AAATTAAAGG	CGGAAGTACG	GTGGTTTCTC	GCAATGTTTC
2301	TTCAATTGAA	GGAAATTGGA	CAATCAGCAA	TAACGCCAAC	GCGACATTTG
2351	GTGTTGTGCC	AAATCAACAA	AATACCATTT	GCACGCGTTC	AGATTGGACA
2401	GGATTAACGA	CTTGTA AAAAC	AGTTAATTTA	ACCGATAAAA	AAGTTATTGA
2451	TTCCATACCG	ACAACACAAA	TTAATGGCTC	TATTAATTTA	ACTAATAATG
2501	CAACAGTGAA	TATTCATGGT	TTAGCAAAAC	TTAATGGTAA	TGTCACTTTA
2551	ATAAATCATA	GCCAATTTAC	ATTGAGCAAC	AATGCCACCC	AAACAGGCAA
2601	TATCCAACCT	TCAAATCACG	CAAATGCAAC	GGTGGATAAT	GCAAACTTGA
2651	ACGGTAATGT	GCATTTAACG	GATTCTGCTC	AATTTTCTTT	AAAAACACGC
2701	CATTTTTTCGC	ACCAAATTCA	GGGCGACAAA	GACACAACAG	TGACGTTGGA
2751	AAATGCGACT	TGGACAATGC	CTAGCGATAC	TACATTGCAG	AATTTAACGC
2801	TAAATAATAG	TACTGTTACG	TTAAATTCAG	CTTATTCAGC	TAGCTCAAAT
2851	AATGCGCCAC	GTCACCGCCG	TTCATTAGAG	ACGGAAACAA	CGCCAACATC
2901	GGAAGAACAT	CGTTTCAACA	CATTGACAGT	AAATGGTAAA	TTGAGCGGGC
2951	AAGGCACATT	CCAATTTACT	TCATCTTTAT	TTGGCTATAA	AAGCGATAAA
3001	ATAAAATTAT	CTAATGACGC	TGAAGGCGAT	TACACATTAG	CTGTTTCGCGA
3051	CACAGGCAAA	GAACCTGTGA	CCCTTGAGCA	ATTAACTTTA	ATTGAAGGCT
3101	TGGATAATCA	ACCCTTGCCA	GATAAGCTAA	AAATTACTTT	AAAAATAAAA
3151	CACGTTGATG	CGGGTG CATG	GCGTTATGAA	TTAGTGAAGA	AAAACGGCGA
3201	ATTCCGCTTG	CATAATCCAA	TAAAAGAGCA	GGAATTGCGC	AATGATTTAG
3251	TAAAAGCAGA	GCAAGTAGAA	CGAGCATTAG	AAGCAAAACA	AGCTGAACTG
3301	ACTACTAAAA	AACAAAAAAC	TGAGGCTAAA	GTGCGGTCAA	AAAGAGCGGC
3351	GTTTTCTGAT	ACCCCGCCTG	ATCAAAGCCA	GTTAAACGCA	TTACAAGCCG
3401	AACTCGAGAC	GATTAATGCC	CAACAGCAAG	TGGCACAAGC	GGTGCAAAAT
3451	CAGAAAGTAA	CTGCACTTAA	CCAAAAGAAC	GAGCAAGTTA	AAACCACTCA
3501	AGATAAAGCA	AATTTAGTCT	TGGCAACTGC	ATTGGTGGAA	AAAGAAACCG
3551	CTCAGATTGA	TTTTGCTAAT	GCAAAATTAG	CTCAGTTGAA	TTTAACACAA
3601	CAACTAGAAA	AAGCCTTAGC	AGTGGCTGAG	CAAGCAGAAA	AAGAGCGTAA
3651	AGCTCAAGAG	CAAGCGAAAA	GACAACGCAA	ACAAAAAGAC	TTGATCAGCC
3701	GTTATTCAAA	TAGTGCGTTA	TCAGAATTAT	CTGCAACAGT	AAATAGTATG
3751	CTTCCCGTTC	AAGATGAATT	AGATCGTCTT	TTTGTAGATC	AAGCTCAATC
3801	TGCGGTGTGG	ACAAATATCT	CACAGGATAA	AAGACGTTAT	GATTCTGATG
3851	CGTTCCGTGC	TTATCAGCAG	AAAACGAACT	TGCGTCAAAT	TGGGGTGCAA
3901	AAAGCCTTAG	CTAACGGACG	AATTGGGGCA	GTTTTCTCGC	ATAGCCGTTC
3951	AGATAATACT	TTTGATGAAC	AGGTTAAAAA	TCACGCAACA	TTAACGATGA
4001	TGTCGGGTTT	TGCCCAATAT	CAATGGGGTG	ATTTACAATT	TGGTGTA AAC
4051	GTGGGAACGG	GAATTAGTGC	GAGTAAAATG	GCTGAAGAAC	AAAGCCGAAA
4101	AATTCATCGA	AAAGCGATAA	ATTATGGCGT	GAATGCAAGT	TATTCGTTCC
4151	ATTTAGGGCA	ATTGGGTATT	CAGCCTTATT	TTGGAGTTAA	TCGCTATTTT
4201	ATTGAACGTA	AAAATTATCA	ATCTGAGGAA	GTGAAAGTGC	AAACACCGAG

Fig. 24B

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4251 CCTTGCATTT AATCGCTATA ATGCTGGAGT ACGGGTCGAT TATACGTTTA
4301 CCCCACACAGA GAATATCAGC GTTAAGCCTT ATTTCTTCGT CAATTATGTT
4351 GATGTTTCAA ACGCTAACGT ACAAACCACT GTAAATCGCG CGGTGTTGCA
4401 ACAACCATTT GGACGTTATT GGCAAAAAGA AGTGGGATTA AAAGCGGAAA
4451 TTTTACATTT CCAACTTTCT GCTTTTATTT CTAAATCTCA AGGTTCGCAA
4501 CTCGGTAAAC AGCGAAATAT GGGCGTGAAA TTAGGATATC GTTGGTAAAA
4551 ATCAACATAA TTTTATTCTA ATAATGGAAC TTTATTTAAT TAAAAGTATC
4601 TAAGTAGCAC CCTATAGGGG ATTAATTAAG AGGATTTAAT AATGAATTTA
4651 ACTAAAATTT TACCCGCATT TGCTGCTGCA GTCGTATTAT CTGCTTGTGC
4701 AAAGGATGCA CCTGAAATGA CAAAATCATC TGCACAAATA GCTGAAATGC
4751 AAACACTTCC AACAATCACT GATAAACAG TTGTATATTC TTGCAATAAA
4801 CAAACTGTGA CTGCAGTGTA TCAATTTG

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Fig. 24C

Amino acid sequence for NTHi strain 1396B Hap protein (first amino acid to last amino acid):

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1  MKKTVFRLNF LTACISLGIV SQAWAGHTYF GIDYQYYRDF AENKGKFTVG
51  AKNIEVYNKN GNLVGTSMTK APMIDFSVVS RNGVAALVGD QYIVSVAHNV
101 GYTNVDFGAE GQNPDQHRFT YKIVKRNNYK NDQTHPYEKD YHNPRLHKFV
151 TEATPIDMTS DMNGNKYTDR TKYPERVRIG SGWQFWRNDQ NNGDQVAGAY
201 HYLTAGNTHN QGGAGGGWSS LSGDVRQAGN YGPIPIAGSS GDSGSPMFIY
251 DAEKQKWLIN GVLRTGNPWA GTENTFQLVR KSFFDEILEK DLRTSFYSPS
301 GNGAYTITDK GDGSGIVKQQ TGRPSEVRIG LKDDKLPAEG KDDVYQYQGP
351 NIYLPRLNNG GNLYFGDQKN GTVTLSTNIN QGAGGLYFEG NFTVSSENNA
401 TWQGAGVHVG EDSTVTWKVN GVENDRLSKI GKGTLHVKAK GENKGSISVG
451 DGKVILEQQA DDQGNKQAFS EIGLVSGRGT VQLNDDKQFN TDKFYFGFRG
501 GRLDLNGHSL TFKRIQNTDE GATIVNHNAT TESTVTITGS DTINDNTGDL
551 TNKRDI AFNG WFGDKDDTKN TGRLNVTYNP LNKDNHFLLS GGTNLKGNIT
601 QDGGTLVFSG RPTPHAYNHL NRLNELGRP K GEVIDDDWI NRTFKAENFQ
651 IKGGSTVVS R NVSSIEGNWT ISNNANATFG VVPNQNTIC TRSDWTGLTT
701 CKTVNLTDKK VIDSIPTTQI NGSINLTNNA TVNIHGLAKL NGNVTLINHS
751 QFTLSNNA TQ TGNIQLSNHA NATVDNANLN GNVHLTDSAQ FSLKNSHFSH
801 QIQGDKDTTV TLENATWTMP SDTTLQNLTL NNSTVTLNSA YSASSNNAPR
851 HRRSLETETT PTSEEH RFNT LTVNGKLSGQ GTFQFTSSLF GYKSDKIKLS
901 NDAEGDYTLA VRDTGKEPVT LEQLTLIEGL DNQPLPKLK ITLKNKHVDA
951 GAWRYELVKK NGEFRLHNPI KEQELRNDLV KAEQVERALE AKQAELT TTKK
1001 QKTEAKVRSK RAAFSDTPPD QSQLNALQAE LETINAQQQV AQAVQNQKVT
1051 ALNQKNEQVK TTQDKANLVL ATALVEKETA QIDFANAKLA QLNLTQQLEK
1101 ALAVAEQAEK ERKAQEQA KR QRKQKDLISR YSNSALS ELS ATVNSMLS VQ
1151 DELDRLFVDQ AQS AVWTNIS QDKRRYDS DA FRAYQQKT NL RQIGVQKALA
1201 NGRIGAVFSH SRSDNTFDEQ VKNHATLTMM SGFAQYQWGD LQFGVNVGTG
1251 ISASKMAEEQ SRKIHRKAIN YGVNASYSFH LGQLGIQPYF GVNRYFIERK
1301 NYQSEEVKVQ TPSLAFNRYN AGVRVDYTFT PTENISVKPY FVNYVDVSN
1351 ANVQTTVNRA VLQQPFGRYW QKEVGLKAEI LHFQLSAFIS KSQGSQ LGKQ
1401 RNMGVKLG YR W

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Fig. 25